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(71) Applicant: EOS BIOTECHNOLOGY, INC. [US/US]; 225A Gateway Boulevard, South San Francisco, CA 94080-7019 (US).		Published <i>Without international search report and to be republished upon receipt of that report.</i>	
(72) Inventors: MACK, David; 2076 Monterey Avenue, Menlo Park, CA 94025 (US). GISH, Kurt, C.; 4302 23rd Street, San Francisco, CA 94114 (US). WILSON, Keith, E.; 219 Jeter Street, Redwood City, CA 94062 (US).			
(74) Agents: BREZNER, David, J. et al.; Flehr Hohbach Test Albritton & Herbert LLP, Suite 3400, 4 Embarcadero Center, San Francisco, CA 94111-4187 (US).			
(54) Title: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER MODULATORS			
(57) Abstract			
<p>Described herein are methods that can be used for diagnosis and prognosis of colorectal cancer. Also described herein are methods that can be used to screen candidate bioactive agents for the ability to modulate colorectal cancer. Additionally, methods and molecular targets (genes and their products) for therapeutic intervention in colorectal and other cancers are described.</p>			

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**NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND  
METHODS OF SCREENING FOR COLORECTAL CANCER MODULATORS**

**FIELD OF THE INVENTION**

5 The invention relates to the identification of expression profiles and the nucleic acids involved in colorectal cancer, and to the use of such expression profiles and nucleic acids in diagnosis and prognosis of colorectal cancer. The invention further relates to methods for identifying and using candidate agents and/or targets which modulate colorectal cancer.

**BACKGROUND OF THE INVENTION**

10 Colorectal cancer is a significant cancer in Western populations. It develops as the result of a pathologic transformation of normal colon epithelium to an invasive cancer. There have been a number of recently characterized genetic alterations that have been implicated in colorectal cancer, including mutations in two classes of genes, tumor-suppressor genes and proto-oncogenes, with recent work suggesting that mutations in DNA repair genes may also be involved in tumorigenesis. For example, inactivating mutations of both alleles of the adenomatous polyposis coli (APC) gene, a  
15 tumor suppressor gene, appears to be one of the earliest events in colorectal cancer, and may even be the initiating event. Other genes implicated in colorectal cancer include the MCC gene, the p53 gene, the DCC (deleted in colorectal carcinoma) gene and other chromosome 18q genes, and genes in the TGF- $\beta$  signaling pathway. For a review, see Molecular Biology of Colorectal Cancer, pp238-299, in Curr. Probl. Cancer, Sept/Oct 1997.

20 Imaging of colorectal cancer for diagnosis has been problematic and limited. In addition, dissemination of tumor cells (metastases) to locoregional lymph nodes is an important prognostic factor; five year survival rates drop from 80 percent in patients with no lymph node metastases to 45 to 50 percent in those patients who do have lymph node metastases. A recent report showed that micrometastases  
25 can be detected from lymph nodes using reverse transcriptase-PCR methods based on the presence of mRNA for carcinoembryonic antigen, which has previously been shown to be present in the vast

majority of colorectal cancers but not in normal tissues. Liefers et al., New England J. of Med. 339(4):223 (1998).

Thus, methods that can be used for diagnosis and prognosis of colorectal cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of colorectal cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate colorectal cancer. Additionally, provided herein are molecular targets for therapeutic intervention in colorectal and other cancers.

#### SUMMARY OF THE INVENTION

The present invention provides methods for screening for compositions which modulate colorectal cancer. Also provided herein are methods of inhibiting proliferation of cell, preferably a colorectal cancer cell. Methods of treatment of cancer, as well as compositions, are also provided herein.

In one aspect, a method of screening drug candidates comprises providing a cell that expresses an expression profile gene or fragments thereof. Preferred embodiments of the expression profile gene are genes which are differentially expressed in cancer cells, preferably colorectal cancer cells, compared to other cells. Preferred embodiments of expression profile genes used in the methods herein include but are not limited to the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9; fragments of the proteins of this group are also preferred. It is understood that molecules for use in the present invention may be from any figure or any subset of listed molecules. Therefore, for example, any one or more of the genes listed above can be used in the methods herein. In another embodiment, a nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.



Also provided herein is a method of screening for a bioactive agent capable of binding to a colorectal cancer modulator protein (CCMP), the method comprising combining the CCMP and a candidate bioactive agent, and determining the binding of the candidate agent to the CCMP. Preferably the CCMP is a protein or fragment thereof selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Further provided herein is a method for screening for a bioactive agent capable of modulating the activity of a CCMP. In one embodiment, the method comprises combining the CCMP and a candidate bioactive agent, and determining the effect of the candidate agent on the bioactivity of the CCMP. Preferably the CCMP is a protein or fragment thereof selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Also provided is a method of evaluating the effect of a candidate colorectal cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the CCMP, or an animal lacking the CCMP, for example as a result of a gene knockout.

Additionally, provided herein is a method of evaluating the effect of a candidate colorectal cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual.

Moreover, provided herein is a biochip comprising a nucleic acid segment which encodes a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably at least two nucleic acid segments are included. In another embodiment, the nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Furthermore, a method of diagnosing a disorder associated with colorectal cancer is provided. The method comprises determining the expression of a gene which encodes a colorectal cancer protein preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9 or a fragment thereof in a first tissue  
5 type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. A difference in the expression indicates that the first individual has a disorder associated with  
10 colorectal cancer.

In another aspect, the present invention provides an antibody which specifically binds to a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7,  
15 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In a preferred embodiment, the fragment of CAA9 is selected from CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS. Other preferred fragments for the breast cancer proteins are shown in the figures. Preferably the antibody is a monoclonal antibody. The antibody can be a fragment of an antibody such as a single stranded  
20 antibody as further described herein, or can be conjugated to another molecule. In one embodiment, the antibody is a humanized antibody.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a colorectal cancer protein (CCMP) or a fragment thereof and an antibody which binds to said CCMP or fragment thereof. In a preferred embodiment, the method comprises combining a CCMP or  
25 fragment thereof, a candidate bioactive agent and an antibody which binds to said CCMP or fragment thereof. The method further includes determining the binding of said CCMP or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the antibody as well as the agent inhibits colorectal cancer.

In a further aspect, a method for inhibiting colorectal cancer is provided. In one embodiment, the method comprises administering to a cell a composition comprising an antibody to a colorectal  
30 modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment

thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. The method can be performed in vitro or in vivo, preferably in vivo to an individual. In a preferred embodiment the method of inhibiting colorectal cancer is provided to an individual with cancer. As described herein, methods of inhibiting colorectal cancer can be performed by administering an inhibitor of colorectal cancer protein activity, including antisense molecules, and preferably small molecules.

Also provided herein are methods eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising a colorectal modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In another aspect, said composition comprises a nucleic acid comprising a sequence encoding a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

A method of neutralizing the effect of a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

In another aspect of the invention, a method of treating an individual for colorectal cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of CJA8. In another embodiment, the method comprises administering to a patient having colorectal cancer an antibody to CJA8 conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

Also provided herein is a method for determining the prognosis of an individual with colorectal cancer comprising determining the level of CJA8 in a sample, wherein a high level of CJA8 indicates a poor prognosis.

Novel sequences are also provided herein. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

#### DETAILED DESCRIPTION OF THE FIGURES

Figure 1 provides the Accession numbers for genes, including expression sequence tags, (incorporated in their entirety here and throughout the application where Accession numbers are provided), upregulated in tumor tissue compared to normal colon tissue.

Figure 2 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 3 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 4 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 5 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

Figure 6 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

- 5      Figure 7 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

Figure 8 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

- 10     Figure 9 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

- 15     Figure 10 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 11 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

- 20     Figure 12 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 13 provides the Accession numbers for genes or fragments thereof, including descriptions of the gene or encoded protein, upregulated in tumor tissue compared to normal colon tissue.

- 25     Figure 14 provides a list of proteins, including Accession numbers for nucleic acid sequences associated with the encoding genes thereof, upregulated in tumor tissue compared to normal colon tissue.

Figure 15 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal protein provided herein, CAA2. The start and stop codon are shaded. The sequence within the two cross marks indicates a preferred novel fragment of CAA2 provided herein, referred to herein as the "CAA2 5' end". Preferred embodiments of CAA2 include at least a portion of the CAA2 5'. The sequence in bold and indicated with a bar at the bottom right beginning with "GGC" and ending with "AAA" can be found in Accession no. AA505133.

Figure 16 shows an embodiment of a nucleic acid encoding CAA2, wherein the start and stop codons are shaded.

Figure 17 shows an embodiment of an amino acid sequence of CAA2. Preferred fragments include at least about 10 amino acids in the N-terminal end. The N-terminus as defined herein includes an embodiment beginning at the first amino acid until about any one of the three amino acids marked with a dot above them. In another embodiment, the N-terminus of CAA2 is defined as the amino acid sequence encoded by the CAA2 5' end.

Figure 18 shows the amino acid sequence of CAA2p1, a preferred CAA2 fragment provided herein.

Figure 19 shows the amino acid sequence of CAA2p2, a preferred CAA2 fragment provided herein.

Figure 20 shows an alignment of the human and mouse CAA2 polypeptides provided herein. The mouse polypeptide contains at least some of the sequence of each of the following Accession numbers: AA386837; A1508773; AA505293; and AA636546.

Figure 21 shows the relative amount of expression of CAA2 in various samples of colon cancer tissue (dark bars) and many normal tissue types (light bars).

Figure 22 shows an embodiment of a colorectal cancer nucleic acid, CAA9 mRNA. The start and stop codons are underlined.

Figure 23 shows the open reading frame of the CAA9 gene wherein the start and stop codons are underlined.

Figure 24 shows an embodiment of the amino acid sequence of a colorectal cancer protein, CAA9, wherein putative transmembrane sequences are underlined. In one embodiment, CAA9 or fragments

of CAA9 are soluble, therefore, the transmembrane domains are deleted, inactivated, and/or the peptide is truncated (with or without re-ligation) to form soluble CAA9.

Figure 25 shows embodiments of colorectal cancer proteins (also termed colorectal cancer modulator proteins). Specifically, Figure 25 shows CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS and their respective solubilities.

Figure 26 shows the relative amount of CAA9 expression in several different samples of colon cancer tissue (dark bars) and normal tissues (light bars).

Figure 27 shows the nucleic acid sequence for the gene encoding CGA7. Start (ATG) and stop (TAG) codons are indicated by shaded boxes. In bold is the sequence of Accession No. AA331393. Underlined is the consensus sequence derived from the compilation and alignment of published est sequences.

Figures 28A and 28B show the alignment summary and descriptions, respectively, of the various est's (by accession number) compiled to generate the consensus sequence of figure 1.

Figure 29 shows the amino acid sequence of CGA7.

Figures 30A and 30B show the relative expression of CGA7 in normal tissue and colon cancer tissue, respectively.

Figure 31 shows the nucleic acid sequence for the mRNA encoding CGA8. Start (ATG) and stop (TAG) codons are indicated by shaded boxes. In bold is the sequence of Accession No. AA2786503. Underlined is the consensus sequence derived from the compilation and alignment of published est sequences.

Figures 32A and 32B show the alignment summary and descriptions, respectively, of the various est's (by accession number) compiled to generate the consensus sequence of figure 1.

Figure 33 shows the amino acid sequence of CGA8.

Figure 34 shows the relative expression of CGA8 in breast cancer tissue, colon cancer tissue, normal tissue and fetal tissue.

Figure 35 shows the sequence for the mRNA encoding CJA8. Start (ATG) and stop (TAA) codons are indicated by shaded boxes.

Figure 36 shows the amino acid sequence for CJA8. A putative transmembrane region is designated by shading. A mouse homolog of this human protein is found at Accession Number AAF21308.1.

- 5      Figure 37 shows the relative amount of expression of CJA8 in several different samples of colon tissues (dark bars) and normal tissues (light bars).

Figure 38 shows the relative amount of expression of BCN7 in several different samples of colon tissues (dark bars) and normal tissues (light bars), as determined using the sequence of Accession Number N22107 as a probe.

- 10     Figure 39 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, BCN7.

Figure 40 shows the sequence for the mRNA encoding CZA8. Start (ATG) and stop (TGA) codons are indicated by underlining.

- 15     Figure 41 shows the sequence for the mRNA encoding BCX2. Start (ATG) and stop (TGA) codons are indicated by underlining.

Figure 42 shows the sequence for the mRNA encoding CBC2. Start (ATG) and stop (TAA) codons are indicated by underlining.

Figure 43 shows the sequence for the mRNA encoding CBC1. Start (ATG) and stop (TGA) codons are indicated by underlining.

- 20     Figure 44 shows the sequence for the mRNA encoding CBC3. Start (ATG) and stop (TGA) codons are indicated by underlining.

Figure 45 shows the sequence for the mRNA encoding BCN5. Start (ATG) and stop (TAA) codons are indicated by underlining.

- 25     Figure 46 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CJA9.



Figure 47 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CQA1.

Figure 48 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CQA2.

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## DETAILED DESCRIPTION OF THE INVENTION

The present invention provides novel methods for diagnosis and prognosis evaluation for colorectal cancer (CRC), as well as methods for screening for compositions which modulate CRC. In one aspect, the expression levels of genes are determined in different patient samples for which either diagnosis or prognosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. That is, normal tissue may be distinguished from CRC tissue, and within CRC tissue, different prognosis states (good or poor long term survival prospects, for example) may be determined. By comparing expression profiles of colon tissue in known different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. The identification of sequences that are differentially expressed in CRC versus normal colon tissue, as well as differential expression resulting in different prognostic outcomes, allows the use of this information in a number of ways. For example, the evaluation of a particular treatment regime may be evaluated: does a chemotherapeutic drug act to improve the long-term prognosis in a particular patient. Similarly, diagnosis may be done or confirmed by comparing patient samples with the known expression profiles. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; for example, screening can be done for drugs that suppress the CRC expression profile or convert a poor prognosis profile to a better prognosis profile. This may be done by making biochips comprising sets of the important CRC genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the CRC proteins can be evaluated for diagnostic and prognostic purposes or to screen candidate agents. In addition, the CRC nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the CRC proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in colorectal cancer, CRC, herein termed "CRC sequences". As outlined below, CRC sequences include those that are up-regulated (i.e. expressed at a higher level) in CRC, as well as those that are down-regulated (i.e. expressed at a lower level) in CRC. In a preferred embodiment, the CRC sequences are from humans; however, as will be appreciated by those in the art, CRC sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other CRC sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc). CRC sequences from other organisms may be obtained using the techniques outlined below.

CRC sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the CRC sequences are recombinant nucleic acids. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid by polymerases and endonucleases, in a form not normally found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e. using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e. through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a CRC protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form

not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

In a preferred embodiment, the CRC sequences are nucleic acids. As will be appreciated by those in the art and is more fully outlined below, CRC sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; for example, biochips comprising nucleic acid probes to the CRC sequences can be generated. In the broadest sense, then, by "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate (Beaucage et al., *Tetrahedron* 49(10):1925 (1993) and references therein; Letsinger, *J. Org. Chem.* 35:3800 (1970); Sprinzl et al., *Eur. J. Biochem.* 81:579 (1977); Letsinger et al., *Nucl. Acids Res.* 14:3487 (1986); Sawai et al., *Chem. Lett.* 805 (1984), Letsinger et al., *J. Am. Chem. Soc.* 110:4470 (1988); and Pauwels et al., *Chemica Scripta* 26:141 (1986)), phosphorothioate (Mag et al., *Nucleic Acids Res.* 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., *J. Am. Chem. Soc.* 111:2321 (1989), O-methylphosphoroamidite linkages (see Eckstein, *Oligonucleotides and Analogues: A Practical Approach*, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, *J. Am. Chem. Soc.* 114:1895 (1992); Meier et al., *Chem. Int. Ed. Engl.* 31:1008 (1992); Nielsen, *Nature*, 365:566 (1993); Carlsson et al., *Nature* 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., *Proc. Natl. Acad. Sci. USA* 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi et al., *Angew. Chem. Intl. Ed. English* 30:423 (1991); Letsinger et al., *J. Am. Chem. Soc.* 110:4470 (1988); Letsinger et al., *Nucleoside & Nucleotide* 13:1597 (1994); Chapters 2 and 3, *ASC Symposium Series* 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., *Bioorganic & Medicinal Chem. Lett.* 4:395 (1994); Jeffs et al., *J. Biomolecular NMR* 34:17 (1994); *Tetrahedron Lett.* 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, *ASC Symposium Series* 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins et al., *Chem. Soc. Rev.* (1995) pp169-176). Several nucleic acid analogs are described in Rawls, *C & E News* June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done for a variety of reasons, for example to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip.

As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

5 Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature ( $T_m$ ) for mismatched versus perfectly matched basepairs. DNA  
10 and RNA typically exhibit a 2-4°C drop in  $T_m$  for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

15 The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand ("Watson") also defines the sequence of the other strand ("Crick"); thus the sequences described herein also includes the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine,  
20 cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

25 A CRC sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the CRC sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

30 The CRC sequences of the invention can be identified as follows. Samples of normal and tumor tissue are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are

commercially available, for example from Affymetrix. Gene expression profiles as described herein are generated, and the data analyzed.

5 In a preferred embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, but not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and placenta. In a preferred embodiment, those genes identified during the CRC screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is preferable that the target be disease specific, to minimize possible side effects.

10 In a preferred embodiment, CRC sequences are those that are up-regulated in CRC; that is, the expression of these genes is higher in colorectal carcinoma as compared to normal colon tissue. "Up-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby  
15 expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al., Nucleic Acids Research 26:1-7 (1998) and <http://www.ncbi.nlm.nih.gov/>. In addition, these genes were found to be expressed in a limited amount or not at all in heart, brain, lung, liver, breast, kidney, prostate, small intestine and spleen.

20 In a preferred embodiment, CRC sequences are those that are down-regulated in CRC; that is, the expression of these genes is lower in colorectal carcinoma as compared to normal colon tissue. "Down-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

25 CRC proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In a preferred embodiment the CRC protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, for example, signaling pathways); aberrant expression of such proteins results in unregulated or dysregulated cellular processes. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity  
30 and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing intracellular proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

In a preferred embodiment, the CRC sequences are transmembrane proteins. Transmembrane proteins are molecules that span the phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Important transmembrane protein receptors include, but are not limited to insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL-1 receptor, IL-2 receptor, etc.

Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid

sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell for example via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

CRC proteins that are transmembrane are particularly preferred in the present invention as they are good targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, for example through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In a preferred embodiment, the CRC proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an

endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. CRC proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, for example for blood tests.

- 5 A CRC sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology to the CRC sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

- 10 As used herein, a nucleic acid is a "CRC nucleic acid" if the overall homology of the nucleic acid sequence to the nucleic acid sequences encoding the amino acid sequences of the figures is preferably greater than about 75%, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. Homology in this context means sequence similarity or identity, with identity being preferred. A preferred comparison for homology purposes is to compare  
15 the sequence containing sequencing errors to the correct sequence. This homology will be determined using standard techniques known in the art, including, but not limited to, the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, PNAS USA 85:2444 (1988), by computerized implementations of these algorithms  
20 (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, WI), the Best Fit sequence program described by Devereux et al., Nucl. Acid Res. 12:387-395 (1984), preferably using the default settings, or by inspection.

- 25 In a preferred embodiment, the sequences which are used to determine sequence identity or similarity are selected from the sequences set forth in the figures, preferably those represented in Figure 12, more preferably those represented in Figures 13A and 13B, still more preferably those of Figures 14-20, 22-25, 27-29, 31-33, 35-37 and 39-48, and fragments thereof. In one embodiment the sequences utilized herein are those set forth in the figures. In another embodiment, the sequences are naturally occurring allelic variants of the sequences set forth in the figures. In another embodiment, the  
30 sequences are sequence variants as further described herein.

One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the



clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, *J. Mol. Evol.* 35:351-360 (1987); the method is similar to that described by Higgins & Sharp *CABIOS* 5:151-153 (1989). Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

5 Another example of a useful algorithm is the BLAST algorithm, described in Altschul et al., *J. Mol. Biol.* 215, 403-410, (1990) and Karlin et al., *PNAS USA* 90:5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul et al., *Methods in Enzymology*, 266: 460-480 (1996); <http://blast.wustl.edu/blast/REACRCE.html>. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters  
10 are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number  
15 of matching identical residues divided by the total number of residues of the "longer" sequence in the aligned region. The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).

Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues of the sequences of the figures.  
20 A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

The alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleosides than those of the figures, it is understood that the percentage of homology will be determined based on the number of homologous nucleosides  
25 in relation to the total number of nucleosides. Thus, for example, homology of sequences shorter than those of the sequences identified herein and as discussed below, will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, for example, nucleic acids which hybridize under high stringency to the nucleic acid sequences which  
30 encode the peptides identified in the figures, or their complements, are considered a CRC sequence. High stringency conditions are known in the art; see for example Maniatis et al., *Molecular Cloning: A Laboratory Manual*, 2d Edition, 1989, and *Short Protocols in Molecular Biology*, ed. Ausubel, et al.,

both of which are hereby incorporated by reference. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T<sub>m</sub>) for the specific sequence at a defined ionic strength pH. The T<sub>m</sub> is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T<sub>m</sub>, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g. 10 to 50 nucleotides) and at least about 60°C for long probes (e.g. greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

In another embodiment, less stringent hybridization conditions are used; for example, moderate or low stringency conditions may be used, as are known in the art; see Maniatis and Ausubel, *supra*, and Tijssen, *supra*.

In addition, the CRC nucleic acid sequences of the invention are fragments of larger genes, i.e. they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, additional sequences of the CRC genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Maniatis et al., and Ausubel, et al., *supra*, hereby expressly incorporated by reference.

Once the CRC nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire CRC nucleic acid. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant CRC nucleic acid can be further-used as a probe to identify and isolate other CRC nucleic acids, for example additional coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant CRC nucleic acids and proteins.

The CRC nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the CRC nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, for example for gene

therapy and/or antisense applications. Alternatively, the CRC nucleic acids that include coding regions of CRC proteins can be put into expression vectors for the expression of CRC proteins, again either for screening purposes or for administration to a patient.

5 In a preferred embodiment, nucleic acid probes to CRC nucleic acids (both the nucleic acid sequences encoding peptides outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the CRC nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be  
10 perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the  
15 target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long,  
20 with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more  
25 probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e. have some sequence in common), or separate.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable  
30 under the conditions of binding, washing, analysis, and removal as outlined below. The binding can be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of either electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent

binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, for example, the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic

acids containing amino groups can be attached to surfaces comprising amino groups, for example using linkers as are known in the art; for example, homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). In addition, in some cases, additional linkers, such as  
5 alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, the oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In an additional embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.  
10

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known  
15 photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

In a preferred embodiment, CRC nucleic acids encoding CRC proteins are used to make a variety of expression vectors to express CRC proteins which can then be used in screening assays, as  
20 described below. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the CRC protein. The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are  
25 suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA  
30 for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the

sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. The transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the CRC protein; for example, transcriptional and translational regulatory nucleic acid sequences from *Bacillus* are preferably used to express the CRC protein in *Bacillus*. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, the transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, the expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The CRC proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a CRC protein, under the appropriate conditions to

induce or cause expression of the CRC protein. The conditions appropriate for CRC protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Drosophila melanogaster* cells, *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, THP1 cell line (a macrophage cell line) and human cells and cell lines.

In a preferred embodiment, the CRC proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral systems. A preferred expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, CRC proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; for example, the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can

include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the CRC protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, CRC proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, CRC protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The CRC protein may also be made as a fusion protein, using techniques well known in the art. Thus, for example, for the creation of monoclonal antibodies, if the desired epitope is small, the CRC protein may be fused to a carrier protein to form an immunogen. Alternatively, the CRC protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the CRC protein is a CRC peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In one embodiment, the CRC nucleic acids, proteins and antibodies of the invention are labeled. By "labeled" herein is meant that a compound has at least one element, isotope or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies or



antigens; and c) colored or fluorescent dyes. The labels may be incorporated into the CRC nucleic acids, proteins and antibodies at any position. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as  $^3\text{H}$ ,  $^{14}\text{C}$ ,  $^{32}\text{P}$ ,  $^{35}\text{S}$ , or  $^{125}\text{I}$ , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Accordingly, the present invention also provides CRC protein sequences. A CRC protein of the present invention may be identified in several ways. "Protein" in this sense includes proteins, polypeptides, and peptides. As will be appreciated by those in the art, the nucleic acid sequences of the invention can be used to generate protein sequences. There are a variety of ways to do this, including cloning the entire gene and verifying its frame and amino acid sequence, or by comparing it to known sequences to search for homology to provide a frame, assuming the CRC protein has homology to some protein in the database being used. Generally, the nucleic acid sequences are input into a program that will search all three frames for homology. This is done in a preferred embodiment using the following NCBI Advanced BLAST parameters. The program is blastx or blastn. The database is nr. The input data is as "Sequence in FASTA format". The organism list is "none". The "expect" is 10; the filter is default. The "descriptions" is 500, the "alignments" is 500, and the "alignment view" is pairwise. The "Query Genetic Codes" is standard (1). The matrix is BLOSUM62; gap existence cost is 11, per residue gap cost is 1; and the lambda ratio is .85 default. This results in the generation of a putative protein sequence.

Also included within one embodiment of CRC proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques known in the art as are outlined above for the nucleic acid homologies.

CRC proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of CRC proteins are portions or fragments of the wild type sequences. herein. In addition, as outlined above, the CRC

nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence, using techniques known in the art.

5 In a preferred embodiment, the CRC proteins are derivative or variant CRC proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative CRC peptide will contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the CRC peptide.

10 Also included in an embodiment of CRC proteins of the present invention are amino acid sequence variants. These variants fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the CRC protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant CRC protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence  
15 variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the CRC protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

20 While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed CRC variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well  
25 known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of CRC protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

30 Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the

molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the CRC protein are desired, substitutions are generally made in accordance with the following chart:

		Chart I	
		Original Residue	Exemplary Substitutions
5	Ala	Ala	Ser
	Arg	Arg	Lys
	Asn	Asn	Gln, His
	Asp	Asp	Glu
10	Cys	Cys	Ser
	Gln	Gln	Asn
	Glu	Glu	Asp
	Gly	Gly	Pro
15	His	His	Asn, Gln
	Ile	Ile	Leu, Val
	Leu	Leu	Ile, Val
	Lys	Lys	Arg, Gln, Glu
20	Met	Met	Leu, Ile
	Phe	Phe	Met, Leu, Tyr
	Ser	Ser	Thr
	Thr	Thr	Ser
25	Trp	Trp	Tyr
	Tyr	Tyr	Trp, Phe
	Val	Val	Ile, Leu
25	Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those shown in Chart I. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the		
30	greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is		
35	substituted for (or by) one not having a side chain, e.g. glycine.		

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analogue, although variants also are selected to modify the characteristics of the CRC proteins as needed. Alternatively, the variant may be designed such that the biological activity of the CRC protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of CRC polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a CRC polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a CRC polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking CRC to a water-insoluble support matrix or surface for use in the method for purifying anti-CRC antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxy-succinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propionimide.

Other modifications include deamidation of glutaminyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the  $\alpha$ -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, *Proteins: Structure and Molecular Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the CRC polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence CRC polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence CRC polypeptide.

Addition of glycosylation sites to CRC polypeptides may be accomplished by altering the amino acid sequence thereof. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence CRC polypeptide (for O-linked glycosylation sites). The CRC amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the CRC polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the CRC polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

Removal of carbohydrate moieties present on the CRC polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of CRC comprises linking the CRC polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

CRC polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a CRC polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a CRC polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the CRC polypeptide. The presence of such epitope-tagged forms of a CRC polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the CRC polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a CRC polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

Also included with the definition of CRC protein in one embodiment are other CRC proteins of the CRC family, and CRC proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related CRC proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the CRC nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art.

In addition, as is outlined herein, CRC proteins can be made that are longer than those depicted in the figures, for example, by the elucidation of additional sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

CRC proteins may also be identified as being encoded by CRC nucleic acids. Thus, CRC proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

In a preferred embodiment, when the CRC protein is to be used to generate antibodies, for example for immunotherapy, the CRC protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller CRC protein will be able to bind to the full length protein. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from CAA2p1 and CAA2p2. In another preferred embodiment, the epitope is selected from CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA89p5 and CAA9p5MAPS.

In one embodiment, the term "antibody" includes antibody fragments, as are known in the art, including Fab, Fab<sub>2</sub>, single chain antibodies (Fv for example), chimeric antibodies, etc., either produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA technologies.

Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the CAA2 or

fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include  
5 Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975).  
10 In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include the CAA2 polypeptide or fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human  
15 origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or  
20 mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the  
25 growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for a CRC protein or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or  
30 receptor subunit, preferably one that is tumor specific.

In a preferred embodiment, the antibodies to CRC are capable of reducing or eliminating the biological function of CRC, as is described below. That is, the addition of anti-CRC antibodies (either polyclonal or preferably monoclonal) to CRC (or cells containing CRC) may reduce or eliminate the CRC activity.

Generally, at least a 25% decrease in activity is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

- In a preferred embodiment the antibodies to the CRC proteins are humanized antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].
- Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol.,



222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., Bio/Technology 10, 779-783 (1992); Lonberg et al., Nature 368 856-859 (1994); Morrison, Nature 368, 812-13 (1994); Fishwild et al., Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995).

By immunotherapy is meant treatment of CRC with an antibody raised against CRC proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen.

In a preferred embodiment the CRC proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted CRC protein.

In another preferred embodiment, the CRC protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the CRC protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane CRC protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the CRC protein. The antibody is also an antagonist of the CRC protein. Further, the antibody prevents activation of the transmembrane CRC protein. In one aspect, when the antibody prevents the binding of other molecules to the CRC protein, the antibody prevents growth of the cell. The antibody also sensitizes

the cell to cytotoxic agents, including, but not limited to TNF-a, TNF-b, IL-1, INF-g and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity. Thus, CRC is treated by administering to a patient antibodies directed against the transmembrane CRC protein.

In another preferred embodiment, the antibody is conjugated to a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the CRC protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the CRC protein. The therapeutic moiety may inhibit enzymatic activity such as protease or protein kinase activity associated with CRC.

In a preferred embodiment, the therapeutic moiety may also be a cytotoxic agent. In this method, targeting the cytotoxic agent to tumor tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with CRC. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against CRC proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane CRC proteins not only serves to increase the local concentration of therapeutic moiety in the CRC afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the CRC protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the CRC protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The CRC antibodies of the invention specifically bind to CRC proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a binding constant in the range of at least  $10^{-4}$ -  $10^{-8}$   $M^{-1}$ , with a preferred range being  $10^{-7}$  -  $10^{-9}$   $M^{-1}$ .

In a preferred embodiment, the CRC protein is purified or isolated after expression. CRC proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the CRC protein may be purified using a standard anti-CRC antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, R., Protein Purification, Springer-Verlag, NY (1982). The degree of purification necessary will vary depending on the use of the CRC protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the CRC proteins and nucleic acids are useful in a number of applications.

In one aspect, the expression levels of genes are determined for different cellular states in the CRC phenotype; that is, the expression levels of genes in normal colon tissue and in CRC tissue (and in some cases, for varying severities of CRC that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be done or confirmed: does tissue from a particular patient have the gene expression profile of normal or CRC tissue.

"Differential expression," or grammatical equivalents as used herein, refers to both qualitative as well as quantitative differences in the genes' temporal and/or cellular expression patterns within and among the cells. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, for example, normal versus CRC tissue. That is, genes may be turned on or turned off in a particular state, relative to another state. As is apparent to the skilled artisan, any comparison of two or more states can be made. Such a qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques in one such state or cell type, but is not detectable in both. Alternatively, the determination is quantitative in that expression is increased or decreased; that is, the expression of the gene is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard

characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, Nature Biotechnology, 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e. upregulation or downregulation), is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably, at least about 200%, with from 300 to at least 1000% being especially preferred.

As will be appreciated by those in the art, this may be done by evaluation at either the gene transcript, or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, for example through the use of antibodies to the CRC protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Thus, the proteins corresponding to CRC genes, i.e. those identified as being important in a CRC phenotype, can be evaluated in a CRC diagnostic test.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well. Similarly, these assays may be done on an individual basis as well.

In this embodiment, the CRC nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of CRC sequences in a particular cell. The assays are further described below in the example.

In a preferred embodiment nucleic acids encoding the CRC protein are detected. Although DNA or RNA encoding the CRC protein may be detected, of particular interest are methods wherein the mRNA encoding a CRC protein is detected. The presence of mRNA in a sample is an indication that the CRC gene has been transcribed to form the mRNA, and suggests that the protein is expressed. Probes to detect the mRNA can be any nucleotide/deoxynucleotide probe that is complementary to and base pairs with the mRNA and includes but is not limited to oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled

5 nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a CRC protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

10 In a preferred embodiment, any of the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in diagnostic assays. This can be done on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

15 As described and defined herein, CRC proteins, including intracellular, transmembrane or secreted proteins, find use as markers of CRC. Detection of these proteins in putative CRC tissue or patients allows for a determination or diagnosis of CRC. Numerous methods known to those of ordinary skill in the art find use in detecting CRC. In one embodiment, antibodies are used to detect CRC proteins. A preferred method separates proteins from a sample or patient by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be any other type of gel including isoelectric focusing gels and the like). Following separation of proteins, the CRC protein is detected by immunoblotting with antibodies raised against the CRC protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

20 In another preferred method, antibodies to the CRC protein find use in in situ imaging techniques. In this method cells are contacted with from one to many antibodies to the CRC protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the CRC protein(s) contains a detectable label. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of CRC proteins. As will be appreciated by one of ordinary skill in the art, numerous other histological imaging techniques are useful in the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

5 In another preferred embodiment, antibodies find use in diagnosing CRC from blood samples. As previously described, certain CRC proteins are secreted/circulating molecules. Blood samples, therefore, are useful as samples to be probed or tested for the presence of secreted CRC proteins. Antibodies can be used to detect the CRC by any of the previously described immunoassay techniques including ELISA, immunoblotting (Western blotting), immunoprecipitation, BIACORE technology and the like, as will be appreciated by one of ordinary skill in the art.

10 In a preferred embodiment, in situ hybridization of labeled CRC nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including CRC tissue and/or normal tissue, are made. In situ hybridization as is known in the art can then be done.

15 It is understood that when comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis as well as a prognosis. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis.

20 In a preferred embodiment, the CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to CRC severity, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, the CRC probes are attached to biochips for the detection and quantification of CRC sequences in a tissue or patient. The assays proceed as outlined for diagnosis.

25 In a preferred embodiment, any of the three classes of proteins as described herein are used in drug screening assays. The CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, Zlokam, et al., Science 279, 84-8 (1998), Heid, 1996 #69.

30 In a preferred embodiment, the CRC proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified CRC proteins are used in screening assays. That is, the present

invention provides novel methods for screening for compositions which modulate the CRC phenotype. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in CRC, candidate bioactive agents may be screened to modulate this gene's response; preferably to down regulate the gene, although in some circumstances to up regulate the gene. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tumor tissue, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4 fold increase in tumor compared to normal tissue, a decrease of about four fold is desired; a 10 fold decrease in tumor compared to normal tissue gives a 10 fold increase in expression for a candidate agent is desired.

As will be appreciated by those in the art, this may be done by evaluation at either the gene or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, for example through the use of antibodies to the CRC protein and standard immunoassays.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well.

In this embodiment, the CRC nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of CRC sequences in a particular cell. The assays are further described below.

Generally, in a preferred embodiment, a candidate bioactive agent is added to the cells prior to analysis. Moreover, screens are provided to identify a candidate bioactive agent which modulates colorectal cancer, modulates CRC proteins, binds to a CRC protein, or interferes between the binding of a CRC protein and an antibody.

The term "candidate bioactive agent" or "drug candidate" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for bioactive agents that are capable of directly or indirectly altering either the CRC phenotype or the expression of a CRC sequence, including both nucleic acid sequences and protein sequences. In preferred embodiments, the bioactive agents modulate the expression profiles, or expression profile nucleic acids or proteins provided herein. In a particularly preferred embodiment, the candidate agent suppresses a CRC phenotype, for example to a normal colon tissue fingerprint. Similarly, the candidate agent preferably suppresses a severe CRC phenotype. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a candidate agent will neutralize the effect of a CRC protein. By "neutralize" is meant that activity of a protein is either inhibited or counter acted against so as to have substantially no effect on a cell.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means. Known pharmacological agents may be subjected to directed or random



chemical modifications, such as acylation, alkylation, esterification, amidification to produce structural analogs.

5 In a preferred embodiment, the candidate bioactive agents are proteins. By "protein" herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. The protein may be made up of naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures. Thus "amino acid", or "peptide residue", as used herein means both naturally occurring and synthetic amino acids. For example, homo-phenylalanine, citrulline and nioreleucine are considered amino acids for the purposes of the invention. "Amino acid" also includes imino acid residues such as proline and hydroxyproline. The side chains may be in either the (R) or  
10 the (S) configuration. In the preferred embodiment, the amino acids are in the (S) or L-configuration. If non-naturally occurring side chains are used, non-amino acid substituents may be used, for example to prevent or retard in vivo degradations.

In a preferred embodiment, the candidate bioactive agents are naturally occurring proteins or fragments of naturally occurring proteins. Thus, for example, cellular extracts containing proteins, or  
15 random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of procaryotic and eucaryotic proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred.

In a preferred embodiment, the candidate bioactive agents are peptides of from about 5 to about 30  
20 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below)  
25 are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any  
30 position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a

defined class, for example, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

5 In a preferred embodiment, the candidate bioactive agents are nucleic acids, as defined above.

As described above generally for proteins, nucleic acid candidate bioactive agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

10 In a preferred embodiment, the candidate bioactive agents are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing the target sequences to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification  
15 such as PCR occurring as needed, as will be appreciated by those in the art. For example, an in vitro transcription with labels covalently attached to the nucleosides is done. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, for example, a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target  
20 sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin.  
25 For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. As known in the art, unbound labeled streptavidin is removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S.  
30 Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670,

5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

5 A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt  
10 concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

15 The reactions outlined herein may be accomplished in a variety of ways, as will be appreciated by those in the art. Components of the reaction may be added simultaneously, or sequentially, in any order, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents may be included in the assays. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Also reagents that otherwise  
20 improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used, depending on the sample preparation methods and purity of the target.

Once the assay is run, the data is analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

25 The screens are done to identify drugs or bioactive agents that modulate the CRC phenotype. Specifically, there are several types of screens that can be run. A preferred embodiment is in the screening of candidate agents that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. That is, candidate agents that can mimic or produce an expression profile in CRC similar to the expression profile of normal colon tissue is expected to result in a suppression of the CRC phenotype. Thus, in this embodiment, mimicking an expression  
30 profile, or changing one profile to another, is the goal.

In a preferred embodiment, as for the diagnosis and prognosis applications, having identified the differentially expressed genes important in any one state, screens can be run to alter the expression of the genes individually. That is, screening for modulation of regulation of expression of a single gene can be done; that is, rather than try to mimic all or part of an expression profile, screening for  
5 regulation of individual genes can be done. Thus, for example, particularly in the case of target genes whose presence or absence is unique between two states, screening is done for modulators of the target gene expression.

In a preferred embodiment, screening is done to alter the biological function of the expression product of the differentially expressed gene. Again, having identified the importance of a gene in a particular  
10 state, screening for agents that bind and/or modulate the biological activity of the gene product can be run as is more fully outlined below.

Thus, screening of candidate agents that modulate the CRC phenotype either at the gene expression level or the protein level can be done.

In addition screens can be done for novel genes that are induced in response to a candidate agent. After identifying a candidate agent based upon its ability to suppress a CRC expression pattern  
15 leading to a normal expression pattern, or modulate a single CRC gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated CRC tissue reveals genes that are not expressed in  
20 normal tissue or CRC tissue, but are expressed in agent treated tissue. These agent specific sequences can be identified and used by any of the methods described herein for CRC genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated CRC tissue sample.

Thus, in one embodiment, a candidate agent is administered to a population of CRC cells, that thus has an associated CRC expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e. a peptide) may be put into a viral  
25 construct such as a retroviral construct and added to the cell, such that expression of the peptide agent is accomplished; see PCT US97/01019, hereby expressly incorporated by reference.  
30

Once the candidate agent has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

- Thus, for example, CRC tissue may be screened for agents that reduce or suppress the CRC phenotype. A change in at least one gene of the expression profile indicates that the agent has an effect on CRC activity. By defining such a signature for the CRC phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.
- 10 In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "CRC proteins" or a "CCMP". In preferred embodiments, the CCMP is as depicted in
- 15 Figures 17-20, 24, 25, 29, 33 and 36, more preferably the protein having the sequence shown in Figures 29 or 36 or encoded by the sequences of Figures 27, 36 and 39-48. The CCMP may be a fragment, or alternatively, be the full length protein to a fragment shown herein. Preferably, the CCMP is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment.
- 20 In a preferred embodiment, the fragment is from CAA9. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the CAA9 fragment has an N-terminal Cys to aid in solubility. Preferably, the fragment is selected from CAA9p1, Caa9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS.
- 25 In a preferred embodiment, the fragment is charged and from the c-terminus of CAA2. In one embodiment, the c-terminus of the fragment is kept as a free acid and the n-terminus is a free amine to aid in coupling, i.e., to cysteine. In another embodiment, the fragment is an internal peptide overlapping hydrophilic stretch of CAA2. In a preferred embodiment, the termini is blocked. Preferably, the fragment of CAA2 is selected from CAA2p1 or CAA2p2. In another preferred embodiment, the fragment is a novel fragment from the N-terminal. In one embodiment, the fragment
- 30 excludes sequence outside of the N-terminal, in another embodiment, the fragment includes at least a portion of the N-terminal. "N-terminal" is used interchangeably herein with "N-terminus" which is further described above.

In one embodiment the CRC proteins are conjugated to an immunogenic agent as discussed herein.  
In one embodiment the CRC protein is conjugated to BSA.

Thus, in a preferred embodiment, screening for modulators of expression of specific genes can be done. This will be done as outlined above, but in general the expression of only one or a few genes are evaluated.

In a preferred embodiment, screens are designed to first find candidate agents that can bind to differentially expressed proteins, and then these agents may be used in assays that evaluate the ability of the candidate agent to modulate differentially expressed activity. Thus, as will be appreciated by those in the art, there are a number of different assays which may be run; binding assays and activity assays.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. In general, this is done as is known in the art. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present.  
Alternatively, cells comprising the CRC proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a CRC protein and a candidate bioactive agent, and determining the binding of the candidate agent to the CRC protein. Preferred embodiments utilize the human CRC protein, although other mammalian proteins may also be used, for example for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative CRC proteins may be used.

Generally, in a preferred embodiment of the methods herein, the CRC protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the

composition and is nondiffusible. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound  
5 material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the CRC protein is bound to the support, and a candidate bioactive agent is added to the assay. Alternatively, the candidate agent is bound to the support and the CRC protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in  
10 screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the candidate bioactive agent to the CRC protein may be done in a  
15 number of ways. In a preferred embodiment, the candidate bioactive agent is labeled, and binding determined directly. For example, this may be done by attaching all or a portion of the CRC protein to a solid support, adding a labeled candidate agent (for example a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as is known in the art.

By "labeled" herein is meant that the compound is either directly or indirectly labeled with a label which provides a detectable signal, e.g. radioisotope, fluorescers, enzyme, antibodies, particles such as  
20 magnetic particles, chemiluminescers, or specific binding molecules, etc. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin etc. For the specific binding members, the complementary member would normally be labeled with a molecule which provides for  
25 detection, in accordance with known procedures, as outlined above. The label can directly or indirectly provide a detectable signal.

In some embodiments, only one of the components is labeled. For example, the proteins (or proteinaceous candidate agents) may be labeled at tyrosine positions using  $^{125}\text{I}$ , or with fluorophores. Alternatively, more than one component may be labeled with different labels; using  $^{125}\text{I}$  for the proteins,  
30 for example, and a fluorophore for the candidate agents.

In a preferred embodiment, the binding of the candidate bioactive agent is determined through the use of competitive binding assays. In this embodiment, the competitor is a binding moiety known to bind to the target molecule (i.e. CRC), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding as between the bioactive agent and the binding moiety, with the binding moiety displacing the bioactive agent.

In one embodiment, the candidate bioactive agent is labeled. Either the candidate bioactive agent, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at any temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are selected for optimum activity, but may also be optimized to facilitate rapid high through put screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the candidate bioactive agent. Displacement of the competitor is an indication that the candidate bioactive agent is binding to the CRC protein and thus is capable of binding to, and potentially modulating, the activity of the CRC protein. In this embodiment, either component can be labeled. Thus, for example, if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the candidate bioactive agent is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the candidate bioactive agent is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the bioactive agent is bound to the CRC protein with a higher affinity. Thus, if the candidate bioactive agent is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the candidate agent is capable of binding to the CRC protein.

In a preferred embodiment, the methods comprise differential screening to identify bioactive agents that are capable of modulating the activity of the CRC proteins. In this embodiment, the methods comprise combining a CRC protein and a competitor in a first sample. A second sample comprises a candidate bioactive agent, a CRC protein and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the CRC protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the CRC protein.



Alternatively, a preferred embodiment utilizes differential screening to identify drug candidates that bind to the native CRC protein, but cannot bind to modified CRC proteins. The structure of the CRC protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect CRC bioactivity are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

5

Positive controls and negative controls may be used in the assays. Preferably all control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, all samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

10

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding.

15

Screening for agents that modulate the activity of CRC proteins may also be done. In a preferred embodiment, methods for screening for a bioactive agent capable of modulating the activity of CRC proteins comprise the steps of adding a candidate bioactive agent to a sample of CRC proteins, as above, and determining an alteration in the biological activity of CRC proteins. "Modulating the activity of CRC" includes an increase in activity, a decrease in activity, or a change in the type or kind of activity present. Thus, in this embodiment, the candidate agent should both bind to CRC proteins (although this may not be necessary), and alter its biological or biochemical activity as defined herein. The methods include both in vitro screening methods, as are generally outlined above, and in vivo screening of cells for alterations in the presence, distribution, activity or amount of CRC proteins.

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25

Thus, in this embodiment, the methods comprise combining a CRC sample and a candidate bioactive agent, and evaluating the effect on CRC activity. By "CRC activity" or grammatical equivalents herein is meant one of the CRC's biological activities, including, but not limited to, cell division, preferably in colon tissue, cell proliferation, tumor growth, transformation of cells. In one embodiment, CRC activity includes activation of CZA8, BCX2, CBC2, CBC1, CBC3, CJA9, BCN5, CQA1, BCN7, CQA2, CJA8,

30

CAA2, CAA9, CGA7 and/or CGA8\*, preferably one of the CRC proteins listed in Figure 14. An inhibitor of CRC activity is the inhibition of any one or more CRC activities.

5 In a preferred embodiment, the activity of the CRC protein is increased; in another preferred embodiment, the activity of the CRC protein is decreased. Thus, bioactive agents that are antagonists are preferred in some embodiments, and bioactive agents that are agonists may be preferred in other embodiments.

10 In a preferred embodiment, the invention provides methods for screening for bioactive agents capable of modulating the activity of a CRC protein. The methods comprise adding a candidate bioactive agent, as defined above, to a cell comprising CRC proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a CRC protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

15 In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, for example hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

20 In this way, bioactive agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the CRC protein. In one embodiment, "colorectal cancer protein activity" as used herein includes at least one of the following: colorectal cancer activity, binding to CJA8, activation of CJA8 or activation of substrates of CJA8 by CJA8. In one embodiment, colorectal cancer activity is defined as the unregulated proliferation of colon tissue, or the growth of cancer in colon tissue. In one aspect, colorectal cancer activity as defined herein is related to the activity of CJA8 in the upregulation of CJA8 in colon cancer tissue.

25 In another embodiment, colorectal cancer protein activity includes at least one of the following: colorectal cancer activity, binding to one of CAA2, CAA9, CGA7 and CGA8, activation of one of CAA2, CAA9, CGA7, and CGA8 or activation of substrates of CAA2, CAA9, CGA7 or CGA8 by CAA2, CAA9, CGA7 or CGA8, respectively. In one preferred embodiment, CAA2 comprises its N-terminal end. In one aspect, colorectal cancer activity as defined herein is related to the activity of CAA2, CAA9, CGA7 and/or CGA8 in the upregulation of CAA2, CAA9, CGA7 and/or CGA8, respectively, in  
30 colon cancer tissue.

In one embodiment, a method of inhibiting colon cancer cell division is provided. The method comprises administration of a colorectal cancer inhibitor.

In another embodiment, a method of inhibiting tumor growth is provided. The method comprises administration of a colorectal cancer inhibitor.

- 5 In a further embodiment, methods of treating cells or individuals with cancer are provided. The method comprises administration of a colorectal cancer inhibitor.

In one embodiment, a colorectal cancer inhibitor is an antibody as discussed above. In another embodiment, the colorectal cancer inhibitor is an antisense molecule. Antisense molecules as used herein include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for colorectal cancer molecules. A preferred antisense molecule is for CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, BCN5, CQA1, BCN7, CQA2, CAA2, CAA9, CGA7 or CGA8, more preferably for the CRC sequences referenced in Figure 14, or for a ligand or activator thereof. A most preferred antisense molecule is for CJA8 or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Antisense molecules may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

- 30 The compounds having the desired pharmacological activity may be administered in a physiologically acceptable carrier to a host, as previously described. The agents may be administered in a variety of

ways, orally, parenterally e.g., subcutaneously, intraperitoneally, intravascularly, etc. Depending upon the manner of introduction, the compounds may be formulated in a variety of ways. The concentration of therapeutically active compound in the formulation may vary from about 0.1-100 wt.%. The agents may be administered alone or in combination with other treatments, i.e., radiation.

- 5 The pharmaceutical compositions can be prepared in various forms, such as granules, tablets, pills, suppositories, capsules, suspensions, salves, lotions and the like. Pharmaceutical grade organic or inorganic carriers and/or diluents suitable for oral and topical use can be used to make up compositions containing the therapeutically-active compounds. Diluents known to the art include aqueous media, vegetable and animal oils and fats. Stabilizing agents, wetting and emulsifying  
10 agents, salts for varying the osmotic pressure or buffers for securing an adequate pH value, and skin penetration enhancers can be used as auxiliary agents.

- Without being bound by theory, it appears that the various CRC sequences are important in CRC. Accordingly, disorders based on mutant or variant CRC genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant CRC genes  
15 comprising determining all or part of the sequence of at least one endogeneous CRC genes in a cell. As will be appreciated by those in the art, this may be done using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the CRC genotype of an individual comprising determining all or part of the sequence of at least one CRC gene of the individual. This is generally done in at least one tissue of the individual, and may include the  
20 evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced CRC gene to a known CRC gene, i.e. a wild-type gene.

- The sequence of all or part of the CRC gene can then be compared to the sequence of a known CRC gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the  
25 sequence between the CRC gene of the patient and the known CRC gene is indicative of a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the CRC genes are used as probes to determine the number of copies of the CRC gene in the genome.

- In another preferred embodiment CRC genes are used as probed to determine the chromosomal  
30 localization of the CRC genes. Information such as chromosomal localization finds use in providing a

diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in CRC gene loci.

Thus, in one embodiment, methods of modulating CRC in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-CRC antibody that reduces or eliminates the biological activity of an endogeneous CRC protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a CRC protein. As will be appreciated by those in the art, this may be accomplished in any number of ways. In a preferred embodiment, for example when the CRC sequence is down-regulated in CRC, the activity of the CRC gene is increased by increasing the amount of CRC in the cell, for example by overexpressing the endogeneous CRC or by administering a gene encoding the CRC sequence, using known gene-therapy techniques, for example. In a preferred embodiment, the gene therapy techniques include the incorporation of the endogenous gene using enhanced homologous recombination (EHR), for example as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, for example when the CRC sequence is up-regulated in CRC, the activity of the endogeneous CRC gene is decreased, for example by the administration of a CRC antisense nucleic acid.

In one embodiment, the CRC proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to CRC proteins, which are useful as described herein. Similarly, the CRC proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify CRC antibodies. In a preferred embodiment, the antibodies are generated to epitopes unique to a CRC protein; that is, the antibodies show little or no cross-reactivity to other proteins. These antibodies find use in a number of applications. For example, the CRC antibodies may be coupled to standard affinity chromatography columns and used to purify CRC proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the CRC protein.

In one embodiment, a therapeutically effective dose of a CRC or modulator thereof is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. As is known in the art, adjustments for CRC degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals, and organisms. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, and in the most preferred embodiment the patient is human.

- 5       The administration of the CRC proteins and modulators of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the CRC proteins and modulators may be directly applied as a solution or spray.
- 10       The pharmaceutical compositions of the present invention comprise a CRC protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or
- 15       otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable
- 20       base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines
- 25       and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

- 30       Additives are well known in the art, and are used in a variety of formulations.

In a preferred embodiment, CRC proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, CRC genes (including both the full-length

sequence, partial sequences, or regulatory sequences of the CRC coding regions) can be administered in gene therapy applications, as is known in the art. These CRC genes can include antisense applications, either as gene therapy (i.e. for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

- 5 In a preferred embodiment, CRC genes are administered as DNA vaccines, either single genes or combinations of CRC genes. Naked DNA vaccines are generally known in the art. Brower, Nature Biotechnology, 16:1304-1305 (1998).

- 10 In one embodiment, CRC genes of the present invention are used as DNA vaccines. Methods for the use of genes as DNA vaccines are well known to one of ordinary skill in the art, and include placing a CRC gene or portion of a CRC gene under the control of a promoter for expression in a CRC patient. The CRC gene used for DNA vaccines can encode full-length CRC proteins, but more preferably encodes portions of the CRC proteins including peptides derived from the CRC protein. In a preferred embodiment a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a CRC gene. Similarly, it is possible to immunize a patient with a plurality of
- 15 CRC genes or portions thereof as defined herein. Without being bound by theory, expression of the polypeptide encoded by the DNA vaccine, cytotoxic T-cells, helper T-cells and antibodies are induced which recognize and destroy or eliminate cells expressing CRC proteins.

- In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to
- 20 the CRC polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are known to those of ordinary skill in the art and find use in the invention.

- In another preferred embodiment CRC genes find use in generating animal models of CRC. As is appreciated by one of ordinary skill in the art, when the CRC gene identified is repressed or diminished in CRC tissue, gene therapy technology wherein antisense RNA directed to the CRC gene
- 25 will also diminish or repress expression of the gene. An animal generated as such serves as an animal model of CRC that finds use in screening bioactive drug candidates. Similarly, gene knockout technology, for example as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence of the CRC protein. When desired, tissue-specific expression or knockout of the CRC protein may be necessary.

- 30 It is also possible that the CRC protein is overexpressed in CRC. As such, transgenic animals can be generated that overexpress the CRC protein. Depending on the desired expression level, promoters

of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of CRC and are additionally useful in screening for bioactive molecules to treat CRC.

- 5 It is understood that the examples described herein in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references and sequences of accession numbers cited herein are incorporated by reference in their entirety.

### EXAMPLES

#### Example 1

#### 10 Tissue Preparation, Labeling Chips, and Fingerprints

##### Purify total RNA from tissue using TRIzol Reagent

- 15 Estimate tissue weight. Homogenize tissue samples in 1ml of TRIzol per 50mg of tissue using a Polytron 3100 homogenizer. The generator/probe used depends upon the tissue size. A generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. Use the 20mm generator for tissue weighing more than 0.6g. If the working volume is greater than 2ml, then homogenize tissue in a 15ml polypropylene tube (Falcon 2059). Fill tube no greater than 10ml.

##### HOMOGENIZATION

- 20 Before using generator, it should have been cleaned after last usage by running it through soapy H<sub>2</sub>O and rinsing thoroughly. Run through with EtOH to sterilize. Keep tissue frozen until ready. Add TRIzol directly to frozen tissue then homogenize.

- 25 Following homogenization, remove insoluble material from the homogenate by centrifugation at 7500 x g for 15 min. in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. Transfer the cleared homogenate to a new tube(s). The samples may be frozen now at -60 to -70°C (and kept for at least one month) or you may continue with the purification.

##### PHASE SEPARATION

Incubate the homogenized samples for 5 minutes at room temperature.  
Add 0.2ml of chloroform per 1ml of TRIzol reagent used in the original homogenization.  
Cap tubes securely and shake tubes vigorously by hand (do not vortex) for 15 seconds.



Incubate samples at room temp. for 2-3 minutes. Centrifuge samples at 6500rpm in a Sorvall superspeed for 30 min. at 4°C. (You may spin at up to 12,000 x g for 10 min. but you risk breaking your tubes in the centrifuge.)

#### RNA PRECIPITATION

- 5 Transfer the aqueous phase to a fresh tube. Save the organic phase if isolation of DNA or protein is desired. Add 0.5ml of isopropyl alcohol per 1ml of TRIzol reagent used in the original homogenization. Cap tubes securely and invert to mix. Incubate samples at room temp. for 10 minutes. Centrifuge samples at 6500rpm in Sorvall for 20min. at 4°C.

#### RNA WASH

- 10 Pour off the supernate. Wash pellet with cold 75% ethanol. Use 1ml of 75% ethanol per 1ml of TRIzol reagent used in the initial homogenization. Cap tubes securely and invert several times to loosen pellet. (Do not vortex). Centrifuge at <8000rpm (<7500 x g) for 5 minutes at 4°C. Pour off the wash. Carefully transfer pellet to an eppendorf tube (let it slide down the tube into the new tube and use a pipet tip to help guide it in if necessary). Depending on the volumes you are
- 15 working with, you can decide what size tube(s) you want to precipitate the RNA in. When I tried leaving the RNA in the large 15ml tube, it took so long to dry (i.e. it did not dry) that I eventually had to transfer it to a smaller tube. Let pellet dry in hood. Resuspend RNA in an appropriate volume of DEPC H<sub>2</sub>O. Try for 2-5ug/ul. Take absorbance readings.

#### Purify poly A<sup>+</sup> mRNA from total RNA or clean up total RNA with Qiagen's

##### RNeasy kit

- 20 Purification of poly A<sup>+</sup> mRNA from total RNA. Heat oligotex suspension to 37°C and mix immediately before adding to RNA. Incubate Elution Buffer at 70°C. Warm up 2 x Binding Buffer at 65°C if there is precipitate in the buffer. Mix total RNA with DEPC-treated water, 2 x Binding Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook. Incubate for 3
- 25 minutes at 65°C. Incubate for 10 minutes at room temperature.

Centrifuge for 2 minutes at 14,000 to 18,000 g. If centrifuge has a "soft setting," then use it. Remove supernatant without disturbing Oligotex pellet. A little bit of solution can be left behind to reduce the loss of Oligotex. Save sup until certain that satisfactory binding and elution of poly A<sup>+</sup> mRNA has occurred.

- 30 Gently resuspend in Wash Buffer OW2 and pipet onto spin column. Centrifuge the spin column at full speed (soft setting if possible) for 1 minute.

Transfer spin column to a new collection tube and gently resuspend in Wash Buffer OW2 and centrifuge as describe herein.

- Transfer spin column to a new tube and elute with 20 to 100 ul of preheated (70°C) Elution Buffer. Gently resuspend Oligotex resin by pipetting up and down. Centrifuge as above. Repeat elution
- 5 with fresh elution buffer or use first eluate to keep the elution volume low.

Read absorbance, using diluted Elution Buffer as the blank.

Before proceeding with cDNA synthesis, the mRNA must be precipitated.

Some component leftover or in the Elution Buffer from the Oligotex purification procedure will inhibit downstream enzymatic reactions of the mRNA.

10 Ethanol Precipitation

Add 0.4 vol. of 7.5 M  $\text{NH}_4\text{OAc}$  + 2.5 vol. of cold 100% ethanol. Precipitate at -20°C 1 hour to overnight (or 20-30 min. at -70°C). Centrifuge at 14,000-16,000 x g for 30 minutes at 4°C. Wash pellet with 0.5ml of 80% ethanol (-20°C) then centrifuge at 14,000-16,000 x g for 5 minutes at room temperature. Repeat 80% ethanol wash. Dry the last bit of ethanol from the pellet in the hood.

- 15 (Do not speed vacuum). Suspend pellet in DEPC  $\text{H}_2\text{O}$  at 1ug/ul concentration.

Clean up total RNA using Qiagen's RNeasy kit

- Add no more than 100ug to an RNeasy column. Adjust sample to a volume of 100ul with RNase-free water. Add 350ul Buffer RLT then 250ul ethanol (100%) to the sample. Mix by pipetting (do not centrifuge) then apply sample to an RNeasy mini spin column. Centrifuge for 15 sec at
- 20 >10,000rpm. If concerned about yield, re-apply flowthrough to column and centrifuge again. Transfer column to a new 2-ml collection tube. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough then centrifuge for 2 min at maximum speed to dry column membrane. Transfer column to a new 1.5-ml collection tube and apply 30-50ul of RNase-free
- 25 water directly onto column membrane. Centrifuge 1 min at >10,000rpm. Repeat elution. Take absorbance reading. If necessary, ethanol precipitate with ammonium acetate and 2.5X volume 100% ethanol.

Make cDNA using Gibco's "SuperScript Choice System for cDNA Synthesis" kit

First Strand cDNA Synthesis

Use 5ug of total RNA or 1ug of polyA+ mRNA as starting material. For total RNA, use 2ul of SuperScript RT. For polyA+ mRNA, use 1ul of SuperScript RT. Final volume of first strand synthesis mix is 20ul. RNA must be in a volume no greater than 10ul. Incubate RNA with 1ul of 100pmol T7-T24 oligo for 10 min at 70C. On ice, add 7 ul of: 4ul 5X 1<sup>st</sup> Strand Buffer, 2ul of 0.1M DTT, and 1 ul of 10mM dNTP mix. Incubate at 37C for 2 min then add SuperScript RT Incubate at 37C for 1 hour.

#### Second Strand Synthesis

Place 1<sup>st</sup> strand reactions on ice.

Add: 91ul DEPC H2O  
 10 30ul 5X 2<sup>nd</sup> Strand Buffer  
 3ul 10mM dNTP mix  
 1ul 10U/ul *E.coli* DNA Ligase  
 4ul 10U/ul *E.coli* DNA Polymerase  
 1ul 2U/ul RNase H

15

Make the above into a mix if there are more than 2 samples. Mix and incubate 2 hours at 16C. Add 2ul T4 DNA Polymerase. Incubate 5 min at 16C. Add 10ul of 0.5M EDTA

#### Clean up cDNA

Phenol:Chloroform:Isoamyl Alcohol (25:24:1) purification using Phase-Lock gel tubes:  
 20 Centrifuge PLG tubes for 30 sec at maximum speed. Transfer cDNA mix to PLG tube. Add equal volume of phenol:chloroform:isamyl alcohol and shake vigorously (do not vortex). Centrifuge 5 minutes at maximum speed. Transfer top aqueous solution to a new tube. Ethanol precipitate: add 7.5X 5M NH4Oac and 2.5X volume of 100% ethanol. Centrifuge immediately at room temp. for 20 min, maximum speed. Remove sup then wash pellet 2X with cold 80% ethanol. Remove  
 25 as much ethanol wash as possible then let pellet air dry. Resuspend pellet in 3ul RNase-free water.

#### In vitro Transcription (IVT) and labeling with biotin

Pipet 1.5ul of cDNA into a thin-wall PCR tube.

#### Make NTP labeling mix:

30 Combine at room temperature: 2ul T7 10xATP (75mM) (Ambion)  
 2ul T7 10xGTP (75mM) (Ambion)  
 1.5ul T7 10xCTP (75mM) (Ambion)

- 5
- |       |        |   |
|-------|--------|---|
| Enzo) | 1.5ul  | T7 10xUTP (75mM) (Ambion)                     |
|       | 3.75ul | 10mM Bio-11-UTP (Boehringer-Mannheim/Roche or |
|       | 3.75ul | 10mM Bio-16-CTP (Enzo)                        |
|       | 2ul    | 10x T7 transcription buffer (Ambion)          |
|       | 2ul    | 10x T7 enzyme mix (Ambion)                    |

Final volume of total reaction is 20ul. Incubate 6 hours at 37C in a PCR machine.

#### RNeasy clean-up of IVT product

Follow previous instructions for RNeasy columns or refer to Qiagen's RNeasy protocol handbook.

- 10 cRNA will most likely need to be ethanol precipitated. Resuspend in a volume compatible with the fragmentation step.

#### Fragmentation

- 15 15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in the fragmentation buffer contributes to precipitation in the hybridization buffer. Fragment RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer.

#### 5 x Fragmentation buffer:

- 200 mM Tris-acetate, pH 8.1  
500 mM KOAc  
20 150 mM MgOAc

The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea of the transcript size range

#### Hybridization

- 25 200 ul (10ug cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 ul or more be made.

Hybridization Mix: fragment labeled RNA (50ng/ul final conc.)

- 5                    50 pM 948-b control oligo  
                      1.5 pM BioB  
                      5 pM BioC  
                      25 pM BioD  
                      100 pM CRE  
                      0.1mg/ml herring sperm DNA  
                      0.5mg/ml acetylated BSA  
                      to 300 ul with 1xMES hyb. buffer

- 10            The instruction manuals for the products used herein are incorporated herein in their entirety.

Labeling Protocol Provided Herein

Hybridization reaction:

Start with non-biotinylated IVT (purified by RNeasy columns)  
 (see example 1 for steps from tissue to IVT)

- 15            IVT antisense RNA; 4 µg:            µl  
                  Random Hexamers (1 µg/µl):    4 µl  
                  H<sub>2</sub>O:                                    µl

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14 µl

- 20            - Incubate 70°C, 10 min. Put on ice.

Reverse transcription:

- 5X First Strand (BRL) buffer: 6 µl  
                  0.1 M DTT:                            3 µl  
                  50X dNTP mix:                        0.6 µl  
                  H<sub>2</sub>O:                                    2.4 µl  
                  Cy3 or Cy5 dUTP (1mM):    3 µl  
                  SS RT II (BRL):                    1 µl

---

16 µl

- 30            - Add to hybridization reaction.  
                  - Incubate 30 min., 42°C.  
                  - Add 1 µl SSII and let go for another hour.

- 50X dNTP mix (25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP: 25  $\mu$ l each of 100mM dATP, dCTP, and dGTP; 10  $\mu$ l of 100mM dTTP to 15  $\mu$ l H<sub>2</sub>O. dNTPs from Pharmacia)

## 5

U-Conn 30

500 µl TE/sample spin at 7000g for 10 min, save flow through for purification

-suspend u-con recovered material in 500µl buffer PB

-proceed w/ normal Qiagen protocol

- Add 1  $\mu$ l of 1/100 dil of DNase/30 $\mu$ l Rx and incubate at 37°C for 15 min.

15      -5 min 95°C to denature enzyme

- Add:

Cot-1 DNA: 10  $\mu$ l

50X dNTPs: 1  $\mu$ l

20

20X SSC: 2.3  $\mu$ l

Na pyro phosphate: 7.5  $\mu$ l

10mg/ml Herring sperm DNA    1ul of 1/10 dilution  
21.8 final vol.

- Dry down in speed vac.

25

- Resuspend in 15  $\mu$ l H<sub>2</sub>O.

- Add 0.38  $\mu$ l 10% SDS.

- Heat 95°C, 2 min.

- Slow cool at room temp. for 20 min.

Put on slide and hybridize overnight at 64°C.

3X SSC/0.03% SDS:

2 min. 37.5 mls 20X SSC+0.75mls 10% SDS in 250mls H<sub>2</sub>O

1X SSC: 5 min.

12.5 mls 20X SSC in 250mls H<sub>2</sub>O

0.2X SSC: 5 min.                      2.5 mls 20X SSC in 250mls H<sub>2</sub>O  
 Dry slides in centrifuge, 1000 RPM, 1min.  
 Scan at appropriate PMT's and channels.

The results are shown in Figures 1 through 11. The lists of genes come from colorectal tumors from a variety of stages of the disease. The genes that are up regulated in the tumors (overall) were also found to be expressed at a limited amount or not at all in the body map. The body map for the colorectal project consists of ten tissues: Heart, Brain, Lung, Liver, Breast, Kidney, Prostate, Small Intestine, Spleen, and Colon. The down regulated genes in tumors (overall) versus normal colon were not selected for their expression or lack of expression in the body map.

As indicated, some of the Accession numbers include expression sequence tags (ESTs). Thus, in one embodiment herein, genes within an expression profile, also termed expression profile genes, include ESTs and are not necessarily full length. Figure 1 shows 51 upregulated genes; Figure 2 shows 194 upregulated genes; Figure 3 shows 1144 upregulated genes and Figure 4 shows 1815 upregulated genes. The genes shown in Figures 1 and 5 are particularly preferred. Figure 5 shows 54 downregulated genes; Figure 6 shows 558 downregulated genes; and Figure 7 shows 1923 downregulated genes; and Figures 8, 9, 10 and 11 provide the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

#### Example 2

Expression studies were performed herein.

As indicated in Figure 21, CAA2 is upregulated in colon cancer tissue. CAA2 is found in chromosome 15, cytoband 15q15-22, interval D15S146-D15S117. CAA2 has N-myristoylation sites and a C-terminal microbody targeting signal. The preferred fragments shown in Figures 18 and 19 have a solubility of 1 mg/ 1 ml H<sub>2</sub>O.

As indicated in Figure 26, CAA9 is upregulated in colon cancer tissue. CAA9 is found in chromosome 5, cytoband 5q23.3, interval D5S471-D5S393.

As indicated in Figures 30A and 30B, CGA7 is upregulated in colon cancer tissue. CGA7 is found in chromosome 2.

As indicated in Figure 34, CGA8 is upregulated in colon cancer tissue.

As indicated in Figure 37, CJA8 is upregulated in colon cancer tissue. CJA8 is found in chromosome 11.

As indicated in Figure 38, BCN7 is upregulated in colon cancer tissue. BCN7 is found in chromosome 5, cytoband 5q22, interval D5S471-D5S393.



## CLAIMS

We claim:

1. A method of screening drug candidates comprising:
  - a) providing a cell that expresses an expression profile gene which encodes a protein selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7 and CQA2 or a fragment thereof;
  - b) adding a drug candidate to said cell; and
  - c) determining the effect of said drug candidate on the expression of said expression profile gene.
2. A method according to claim 1 wherein said determining comprises comparing the level of expression in the absence of said drug candidate to the level of expression in the presence of said drug candidate, wherein the concentration of said drug candidate can vary when present, and wherein said comparison can occur after addition or removal of the drug candidate.
3. A method according to claim 1 wherein the expression of said profile gene is decreased as a result of the introduction of the drug candidate.
4. A method of screening for a bioactive agent capable of binding to a colorectal cancer modulator protein (CCMP), wherein said CCMP is CJA8 or a fragment thereof, said method comprising combining said CCMP and a candidate bioactive agent, and determining the binding of said candidate agent to said CCMP.
5. A method for screening for a bioactive agent capable of modulating the activity of a colorectal cancer modulator protein (CCMP), wherein said CCMP is CJA8 or a fragment thereof, said method comprising combining said CCMP and a candidate bioactive agent, and determining the effect of said candidate agent on the bioactivity of said CCMP.
6. A method of evaluating the effect of a candidate colorectal cancer drug comprising:
  - a) administering said drug to a patient;
  - b) removing a cell sample from said patient; and
  - c) determining the expression profile of said cell.
7. A method according to claim 6 further comprising comparing said expression profile to an expression profile of a healthy individual.

8. A biochip comprising a nucleic acid segment encoding CJA81 or a fragment thereof, wherein said biochip comprises fewer than 1000 nucleic acid probes.
9. A method of diagnosing colorectal cancer comprising:  
a) determining the expression of a gene encoding CJA8 or a fragment thereof in a first tissue type of a first individual; and  
b) comparing said expression of said gene from a second normal tissue type from said first individual or a second unaffected individual;  
wherein a difference in said expression indicates that the first individual has colorectal cancer.
10. An antibody which specifically binds to CJA8, or a fragment thereof.
11. An antibody which specifically binds to CAA9, or a fragment thereof.
12. The antibody of Claim 11 wherein said fragment is selected from the group CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS.
13. The antibody of Claim 10, wherein said antibody is a monoclonal antibody.
14. The antibody of Claim 10, wherein said antibody is a humanized antibody.
15. The antibody of Claim 10, wherein said antibody is an antibody fragment.
16. A method for screening for a bioactive agent capable of interfering with the binding of a colorectal cancer modulator protein (CCMP) or a fragment thereof and an antibody which binds to said CCMP or fragment thereof, said method comprising:  
a) combining a CCMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said CCMP or fragment thereof; and  
b) determining the binding of said CCMP or fragment thereof and said antibody.
17. A method for inhibiting colorectal cancer, said method comprising administering to a cell a composition comprising an antibody to CJA8 or a fragment thereof.
18. The method of Claim 17 wherein said cell is a cell of an individual.
19. The method of Claim 18 wherein said individual has cancer.

20. The method of Claim 17 wherein said antibody is a humanized antibody.
21. The method of Claim 17 wherein said antibody is an antibody fragment.
22. A method for inhibiting colorectal cancer in a cell, wherein said method comprises administering to a cell a composition comprising antisense molecules to CJA8.
- 5 23. A peptide consisting essentially of CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 or CAA9p5MAPS.
24. A composition comprising the peptide of Claim 23.
25. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising CJA8 or a fragment thereof.
- 10 26. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising a nucleic acid comprising a sequence encoding CJA8 or a fragment thereof.
27. A composition capable of eliciting an immune response in an individual, said composition comprising CJA8 or a fragment thereof and a pharmaceutically acceptable carrier.
- 15 28. A composition capable of eliciting an immune response in an individual, said composition comprising a nucleic acid comprising a sequence encoding CJA8 or a fragment thereof and a pharmaceutically acceptable carrier.
29. A method of treating an individual for colorectal cancer comprising administering to said individual an inhibitor of CJA8.
- 20 30. The method of Claim 29 wherein said inhibitor is an antibody.
31. A method for determining the prognosis of an individual with colorectal cancer comprising determining the level of CJA8 in a sample, wherein a high level of CJA8 indicates a poor prognosis.

32. A method of neutralizing the effect of a CJA8, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization.
- 5 33. A method for localizing a therapeutic moiety to colorectal cancer tissue comprising exposing said tissue to an antibody to CJA8 or fragment thereof conjugated to said therapeutic moiety.
34. The method of Claim 33, wherein said therapeutic moiety is a cytotoxic agent.
35. The method of Claim 33, wherein said therapeutic moiety is a radioisotope.
- 10 36. A method of treating colorectal cancer comprising administering to an individual having colorectal cancer an antibody to CJA8 or fragment thereof conjugated to a therapeutic moiety.
37. The method of Claim 36, wherein said therapeutic moiety is a cytotoxic agent.
38. The method of Claim 36, wherein said therapeutic moiety is a radioisotope.

## FIGURE 1

Primary Key	fold upregulated in Tumor over normal colon	Accession	Unigene CLUSTER	Unigene Descriptor
37677	>10	AA460530	Hs.98384	Homo sapiens orphan G protein-coupled receptor HG38 mRNA complete cds
6449	>10	X89986	Hs.32936	H.sapiens mRNA for NBK apoptotic inducer protein
4178	>10	U30246	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
18330	>10	AA216722	Hs.54481	Human mRNA for apolipoprotein E receptor 2 complete cds
5692	>10	X17644	Hs.2707	G1 to S phase transition 1
16810	>10	AA053636	Hs.129849	PBK1
33109	>10	W59961	Hs.22564	Human mRNA for KIAA0389 gene complete cds
37246	>10	AA449311	Hs.98558	Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds
2857	>10	M58597	Hs.2173	Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific)
14338	>10	AA598712	Hs.23723	ESTs Weakly similar to ORF YPL212c [S cerevisiae]
4876	9.6	U55206	Hs.78619	Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA complete cds
2192	7.8	L48211	Hs.20954	Homo Sapiens angiotensin II receptor gene complete cds
5793	7.4	X54942	Hs.83758	CDC28 protein kinase 2
18231	6.3	AA199747	Hs.79025	Human mRNA for KIAA0096 gene partial cds
6061	6.1	X68314	Hs.2704	Glutathione peroxidase 2 gastrointestinal
27117	5.0	AA405098	Hs.38178	ESTs Weakly similar to MOESIN/VEZRN/RADIXIN HOMOLOG [D.melanogaster]
12669	5.0	AA417030	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
1106	4.8	HG2981-HT3127	EST - HG2981-HT3127	
2157	4.6	L41939	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds
13193	4.4	AA442763	Hs.20483	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]
5690	4.4	X17620	Hs.118638	NUCLEOSIDE DIPHOSPHATE KINASE A
28050	4.1	AA479139	Hs.75393	Acid phosphatase 1 soluble
4540	3.5	U48807	Hs.23359	Human MAP kinase phosphatase (MKP-2) mRNA complete cds
26105	3.1	AA243133	Hs.48915	Homo sapiens serine/threonine kinase (BTAK) mRNA complete cds
19177	3.1	H10994	Hs.12338	ESTs
5780	3.1	X54489	Hs.789	GRO1 oncogene (melanoma growth stimulating activity alpha)
33620	3.0	W93943	Hs.59509	ESTs
4536	2.9	U48705	Hs.75562	Receptor protein-tyrosine kinase EDDR1
5928	2.9	X62048	Hs.75188	WEE1-LIKE PROTEIN KINASE
28258	2.8	AA505133	Hs.62273	ESTs
21256	2.7	R09195	Hs.151385	Homo sapiens mRNA for KIAA0564 protein partial cds

## FIGURE 1 (CONT.)

27748	2.5	AA453159	Hs.41723	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds
25310	2.5	AA046745	Hs.110457	ESTs
2640	2.4	M30448	EST - M30448	
3834	2.3	U12595	Hs.2204	Human tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA partial cds
4674	2.3	U54999	Hs.93121	Human LGN protein mRNA complete cds
5769	2.3	X53800	Hs.89690	GRO3 oncogene
25050	2.3	AA011134	Hs.25863	ESTs Weakly similar to renin [H.sapiens]
41935	2.3	T29681	Hs.75761	Human serine kinase mRNA complete cds
26895	2.3	AA292765	Hs.42650	H.sapiens mRNA for M-phase phosphoprotein mpp5
1782	2.1	L12711	Hs.89843	Transketolase (Wernicke-Korsakoff syndrome)
25583	2.1	AA113149	Hs.8130	Homo sapiens IPL (IPL) mRNA complete cds
1487	1.8	J03934	Hs.60706	NAD(P)H:menadione oxidoreductase
7656	1.5	AA203428	Hs.7756	ESTs Moderately similar to ANKYRIN BRAIN VARIANT 2 [Homo sapiens]
683	1.5	D79997	Hs.41697	Human mRNA for KIAA0175 gene complete cds
836	1.5	D87444	Hs.79305	Human mRNA for KIAA0255 gene complete cds
3098	1.2	M77836	Hs.79217	PYRROLINE-5-CARBOXYLATE REDUCTASE
6879	1.1	Z29066	Hs.80896	H.sapiens nek2 mRNA for protein kinase
6880	1.0	Z29067	Hs.2236	H.sapiens nek3 mRNA for protein kinase
2473	0.7	M21904	Hs.79748	Antigen identified by monoclonal antibodies 4F2 TRA1.10 TROP4 and T43
36508	0.7	AA429621	Hs.79093	Human 100 kDa coactivator mRNA complete cds

FIGURE 2

Primary Key	fold upregulated of Tumor	Accession	Unigene CLUSTER	Unigene Descriptor
33616	>10	W93726	Hs.55279	Protease inhibitor 5 (maspin)
34197	>10	AA232315	Hs.12540	Homo sapiens clone 23797 and 23917 mRNA partial cds
19387	>10	H20128	Hs.31656	ESTs
8125	>10	AA330771	Hs.82911	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence
18362	>10	AA223912	Hs.12013	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor
39995	>10	H62474	Hs.108240	EST
19328	>10	H17808	Hs.22858	ESTs
38590	>10	AA598648	Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
38456	>10	AA504343	Hs.101074	ESTs
17559	>10	AA128407	Hs.71190	ESTs
5619	>10	X14850	Hs.2711	HISTONE H2A.X
4029	>10	U21050	Hs.74598	Human DNA polymerase delta small subunit mRNA complete cds
15006	>10	U30246	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
3659	>10	U04313	Hs.55279	Protease inhibitor 5 (maspin)
26916	>10	AA331393	Hs.47378	ESTs
1346	>10	HG4716-HT5158	EST - HG4716-HT5158	
37491	10.0	AA455239	Hs.87630	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 (Caenorhabditis elegans)
13110	9.8	AA435840	Hs.19114	Homo sapiens mRNA for high mobility group protein HMG2a
4676	9.8	U55206	Hs.78619	Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA complete cds
21655	8.7	R38239	Hs.25276	EST
14723	8.3	D59894	Hs.34782	ESTs
5793	7.4	X54942	Hs.83758	CDC28 protein kinase 2
29848	7.1	N22107	Hs.124215	ESTs
9347	7.0	H03686	Hs.112013	ESTs
6078	7.0	X69141	Hs.48876	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE
9326	6.8	D89377	Hs.89404	Msh (Drosophila) homeo box homolog 2
1566	6.7	J05614	EST - J05614	
25675	6.7	AA129757	Hs.54602	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]
20126	6.4	N22015	Hs.18457	ESTs
6061	6.1	X68314	Hs.2704	Glutathione peroxidase 2 gastrointestinal
10867	6.1	AA088458	Hs.19322	ESTs Weakly similar to 3LU SUBFAMILY J1
18062	6.0	AA179845	Hs.73625	ESTs Moderately similar to rabkinin-6 [M.musculus]
4093	5.9	U25182	Hs.83383	Human antioxidant enzyme AOE37-2 mRNA complete cds
18290	5.8	AA211901	Hs.86430	ESTs
5330	5.8	U91327	EST - U91327	
4244	5.7	U33286	Hs.90073	Human chromosome segregation gene homolog CAS mRNA complete cds

## FIGURE 2 (CONT.)

6928	5.7	Z46629	Hs.2316	SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversal)
6160	5.0	X74794	Hs.89699	CDC21 HOMOLOG
31487	5.4	N69507	Hs.129849	ESTs
9470	5.3	H46617	EST - H46617	
33458	5.0	W86835	Hs.14158	Homo sapiens mRNA for KIAA0636 protein complete cds
12669	5.0	AA417030	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
1106	4.8	HG2981-HT3127	EST - HG2981-HT3127	
34367	4.8	AA251758	Hs.40323	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA complete cds
11595	4.8	AA242819	Hs.32539	ESTs
17622	4.8	AA131594	Hs.71435	ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]
34754	4.7	AA287642	Hs.81848	Human mRNA for KIAA0078 gene complete cds
25038	4.7	AA010065	Hs.83758	CDC28 protein kinase 2
5312	4.6	U90716	Hs.79187	Human cell surface protein HCAR mRNA complete cds
8085	4.6	AA314779	Hs.105484	ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
33656	4.0	W95477	Hs.50582	ESTs
8264	4.5	AA401334	Hs.106941	ESTs
34479	4.5	AA262080	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
7898	4.4	AA263032	Hs.81634	ESTs
10716	4.4	AA053319	Hs.9951	ESTs
5690	4.4	X17620	Hs.118638	NUCLEOSIDE DIPHOSPHATE KINASE A
20203	4.3	N25855	Hs.5858	ESTs Moderately similar to III ALU SUBFAMILY SQ WARNING ENTRY III [H.sapiens]
10923	4.2	AA116036	Hs.9329	ESTs
28050	4.1	AA479139	Hs.75393	Acid phosphatase 1 soluble
10970	4.1	AA129390	Hs.5285	ESTs
4149	4.1	U28386	Hs.2397	RAG (recombination activating gene) cohort 1
5767	4.1	X53793	Hs.118226	MULTIFUNCTIONAL PROTEIN ADE2
26596	4.0	AA279943	Hs.88671	ESTs
8961	3.9	AFFX-	AFFX-HUMTFRRM11507_3	
36604	3.9	AA598803	Hs.111496	ESTs
30560	3.9	N49284	Hs.1334	MYB PROTO-ONCOGENE PROTEIN
8513	3.8	AA446990	Hs.103135	ESTs
14509	3.8	AA609943	Hs.32793	ESTs
25284	3.8	AA045074	Hs.110146	ESTs Weakly similar to 52-kD SS-A/Ro autoantigen [H.sapiens]
27354	3.8	AA425221	Hs.81688	ESTs
18385	3.8	AA227219	Hs.110826	Homo sapiens CAGF9 mRNA partial cds
25240	3.7	AA039713	Hs.110406	ESTs
16854	3.7	AA055552	Hs.71622	ESTs Weakly similar to KIAA0319 [H.sapiens]
3709	3.7	U07550	Hs.1197	Heat shock 10 kD protein 1 (chaperonin 10)
13606	3.5	AA456437	Hs.20386	ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT [H.sapiens]
8338	3.4	AA417152	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds



## FIGURE 2 (CONT.)

387	D28589	EST - D28589	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]
15643	W58247	Hs.27437	ESTs
13838	AA465342	Hs.34045	Basic transcription element binding protein 2
251	D14520	Hs.84728	Zinc finger protein 139 (clone pHZ-37)
3778	U09848	Hs.363	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE
5660	X16396	Hs.37791	ESTs
17365	AA101551	Hs.68900	Homo sapiens importin beta subunit mRNA complete cds
33985	AA181580	Hs.81690	ESTs
19233	H12634	Hs.8104	ESTs
13767	AA463234	Hs.119387	Human FX protein mRNA complete cds
4738	U58766	Hs.75801	EST - RC_AA070364
17041	AA070364	Hs.44131	ESTs
15504	W28362	Hs.55682	Human translation initiation factor eIF3 p66 subunit mRNA complete cds
7401	AA094800	Hs.36454	ESTs Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]
18883	F04258	Hs.125123	ESTs Weakly similar to IIII ALU SUBFAMILY . [H.sapiens]
23930	T96690	Hs.25916	ESTs
11288	AA198512	Hs.82962	Thymidylate synthase
170	D00596	Hs.36708	Homo sapiens MAO3-like protein kinase mRNA complete cds
11659	AA251909	Hs.3566	ESTs Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]
14134	AA489080	Hs.11817	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae]
11140	AA158132	Hs.31730	Homo sapiens RRM RNA binding protein Gry-1bp (GRY-RBP) mRNA complete cds
17925	AA164209	Hs.73291	ESTs
26530	AA278650	Hs.110048	ESTs
7445	AA104023	Hs.73596	ESTs
18055	AA179387	Hs.87246	Human Bcl-2 binding component 3 (bbc3) mRNA partial cds
15174	U82987	Hs.59509	ESTs
33620	W93943	Hs.75839	Human (p23) mRNA complete cds
1932	L24804	Hs.3657	ESTs
39556	F03738	Hs.79070	V-myc avian myelocytomatosis viral oncogene homolog
1605	L00058	Hs.75562	Receptor protein-tyrosine kinase EDDR1
4536	U48705	Hs.107213	ESTs
36200	AA421164	Hs.22595	ESTs
12313	AA397916	Hs.15641	ESTs
19867	H61476	Hs.82685	CD47 antigen (Rh-related antigen integrin-associated signal transducer)
6081	X69398	Hs.62663	ESTs
16708	AA043944	Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
357	D26156	Hs.5080	ESTs Weakly similar to T04A8.11 [C.elegans]
8059	AA310967	Hs.139386	ESTs
35830	AA411448	Hs.6831	Homo sapiens clone 1400 unknown protein mRNA partial cds
20151	N22895		

## FIGURE 2 (CONT.)

28258	AA505133	2.8	Hs.62273	ESTs	
8816	AA460077	2.8	Hs.28555	ESTs	
6480	X91788	2.8	Hs.84974	H.sapiens mRNA for lcn protein	
14566	AA621122	2.8	Hs.5198	ESTs	
14182	AA490885	2.8	Hs.21766	ESTs	
35955	AA412528	2.7	Hs.20183	ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [R.norvegicus]	
17642	AA132983	2.7	Hs.44155	ESTs Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [H.sapiens]	
6131	X72841	2.7	Hs.2758	Human retinoblastoma-binding protein (RbAp48) mRNA complete cds	
6444	X89750	2.7	Hs.90077	H.sapiens mRNA for TGIF protein	
7701	AA215333	2.7	Hs.97101	ESTs	
42534	W73189	2.7	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds	
34796	AA291259	2.7	Hs.97101	ESTs	
1923	L23808	2.7	Hs.1695	Matrix metalloproteinase 12 (macrophage elastase)	
10951	AA126719	2.8	Hs.25282	ESTs	
11308	AA207114	2.8	Hs.27842	ESTs	
4086	U24704	2.6	Hs.111709	Human antiseptory factor-1 mRNA complete cds	
5587	X13482	2.6	Hs.80506	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'	
19841	H59617	2.6	Hs.5199	ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Drosophila melanogaster]	
7614	AA187579	2.8	Hs.102696	ESTs Weakly similar to Yel007c-ap [S.cerevisiae]	
11362	AA227261	2.8	Hs.20922	ESTs	
13866	AA476319	2.6	Hs.5327	ESTs	
2993	M64929	2.6	Hs.75200	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform	
12986	AA430032	2.6	Hs.7487	ESTs Moderately similar to PTTG gene product [R.norvegicus]	
5932	X62153	2.5	Hs.82479	Minichromosome maintenance deficient (S. cerevisiae) 3	
38434	AA497013	2.5	Hs.142592	ESTs	
38185	AA487508	2.5	Hs.9877	Homo sapiens mRNA for KIAA0688 protein complete cds	
1424	J02845	2.5	Hs.81613	Eukaryotic translation initiation factor 2A	
21876	R43286	2.5	EST - RC_R43286		
6485	X92098	2.5	Hs.75914	H.sapiens mRNA for transmembrane protein mp24	
7960	AA285277	2.4	Hs.8932	Homo sapiens brain expressed ring finger protein mRNA complete cds	
452	D38076	2.4	Hs.24763	RAN binding protein 1	
11701	AA253031	2.4	Hs.31730	Homo sapiens RRM RNA binding protein Gyr-rbp (GRY-RBP) mRNA complete cds	
36390	AA426291	2.4	Hs.108527	ESTs Weakly similar to No definition line found [C.elegans]	
14420	AA600322	2.4	Hs.19574	ESTs Highly similar to AAC-RICH MRNA CLONE AAC3 PROTEIN [Dictyostellum discoideum]	
6387	X85372	2.4	Hs.105465	H.sapiens mRNA for Sm protein F	
1497	J04088	2.4	Hs.3378	Topoisomerase (DNA) II alpha (170KD)	
27872	AA459254	2.4	Hs.48855	ESTs	
8163	AA357394	2.4	Hs.98073	ESTs	
23065	T23539	2.4	Hs.7165	ESTs Highly similar to zinc finger protein [M.musculus]	
20837	N69263	2.4	Hs.20524	ESTs Highly similar to HEXOKINASE TYPE I [Homo sapiens]	

## FIGURE 2 (CONT.)

17352	2.3	AA100925	Hs.20990	ESTs	EST - RC_D51272_s
28796	2.3	D51272	Hs.4310	ESTs	ESTs
26679	2.3	AA281733	Hs.14611	ESTs	Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds
24092	2.3	W42845	Hs.83532	ESTs	Membrane cofactor protein (CD46 trophoblast-lymphocyte cross-reactive antigen)
5675	2.3	X59405	Hs.7381	ESTs	Homo sapiens voltage dependent anion channel protein mRNA complete cds
7404	2.3	AA094989	Hs.77496	ESTs	H.sapiens mRNA for Sm protein G
6388	2.3	X85373	Hs.25863	ESTs	ESTs Weakly similar to renin [H.sapiens]
25050	2.3	AA011134	Hs.75761	ESTs	Human serine kinase mRNA complete cds
41935	2.3	T29681	Hs.21486	ESTs	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA
3343	2.3	M97936	Hs.80684	ESTs	High-mobility group (nonhistone chromosomal) protein 2
5937	2.2	X62534	Hs.71475	ESTs	ESTs
7387	2.2	AA093977	Hs.5683	ESTs	Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds
20843	2.2	N69352	Hs.76887	ESTs	Human 26S proteasome-associated pab1 homolog (POH1) mRNA complete cds
28448	2.2	AA621752	Hs.103300	ESTs	EST - D78129
651	2.2	D78129	Hs.21214	ESTs	Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds
11688	2.2	AA252672	Hs.1334	ESTs	MYB PROTO-ONCOGENE PROTEIN
11803	2.2	AA257971	Hs.27931	ESTs	ESTs
4046	2.2	U22376	Hs.104058	ESTs	ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MER2-CPRT INTERGENIC REGION [Saccharomyces cerevisiae]
20276	2.2	N32919	Hs.10600	ESTs	ESTs Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION [Saccharomyces cerevisiae]
34370	2.1	AA251829	EST - S75256	EST - S75256	
14562	2.1	AA621340	EST - HG1112-HT1112	EST - HG1112-HT1112	
3461	2.1	S75256	Hs.77899	ESTs	Tropomyosin alpha chain (skeletal muscle)
924	2.1	HG1112-HT1112	Hs.15313	ESTs	ESTs Weakly similar to PRE-MRNA SPLICING HELICASE BRR2 [S.cerevisiae]
24348	2.1	W86469	Hs.78770	ESTs	Isoleucine-tRNA synthetase
10998	2.1	AA112063	Hs.10724	ESTs	ESTs Weakly similar to unknown [S.cerevisiae]
381	2.1	D28473	Hs.8130	ESTs	Homo sapiens IPL (iPL) mRNA complete cds
11528	2.1	AA236018	Hs.107213	ESTs	ESTs
25593	2.1	AA113149	Hs.83550	ESTs	Human heterochromatin protein HP1-Hs-gamma mRNA complete cds
38040	2.1	AA481403	Hs.83379	ESTs	Cytochrome c oxidase subunit VIb
4111	2.1	U28312	Hs.89866	ESTs	Coproporphyrinogen oxidase (coproporphyrin harderoporphyria)
61	2.0	AC002115	EST - D28423	EST - D28423	
9112	2.0	D16611	EST - D28364	EST - D28364	
380	2.0	D28423	Hs.42582	ESTs	ESTs
377	2.0	D28364	Hs.5950	ESTs	ESTs
28379	2.0	AA609710	Hs.9564	ESTs	Human clone 121711 defective mariner transposon Hsma2 mRNA sequence
24230	2.0	W72276	Hs.104558	ESTs	ESTs
40212	2.0	H88535			
8118	2.0	AA328993			

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## FIGURE 3 (CONT.)

5071	U73524	Hs 87485	Human putative ATPGTP-binding protein (HEA) mRNA complete cds
4994	U72514	Hs 12045	Human C21 mRNA complete cds
26355	AA256378	Hs 99291	ESTs
4455	U49944	Hs 14732	MALATE OXIDOREDUCTASE
10748	AA055382	Hs 14540	ESTs
6111	AC322787	Hs 4770	ESTs
32183	U04041	Hs 22253	ESTs
38970	AA055382	Hs 117239	ESTs
21519	AA190868	Hs 12013	ESTs
54013	X16987	Hs 11878	ESTs
41107	U04041	Hs 11878	ESTs
5996	U04041	Hs 11878	ESTs
10023	AA249032	Hs 18349	ESTs
40498	N25096	Hs 135991	ESTs
6315	X16987	Hs 16381	ESTs
4702	U57341	Hs 27853	ESTs
16978	U04041	Hs 17548	ESTs
24197	U04041	Hs 17548	ESTs
4713	U04041	Hs 17548	ESTs
38460	U04041	Hs 17548	ESTs
10326	U04041	Hs 17548	ESTs
42786	U04041	Hs 17548	ESTs
34011	U04041	Hs 17548	ESTs
16935	U04041	Hs 17548	ESTs
8364	U04041	Hs 17548	ESTs
29893	U04041	Hs 17548	ESTs
36553	U04041	Hs 17548	ESTs
11160	U04041	Hs 17548	ESTs
1156	U04041	Hs 17548	ESTs
31736	U04041	Hs 17548	ESTs
11815	U04041	Hs 17548	ESTs
5797	U04041	Hs 17548	ESTs
5798	U04041	Hs 17548	ESTs
10993	U04041	Hs 17548	ESTs
11654	U04041	Hs 17548	ESTs
20057	U04041	Hs 17548	ESTs
39436	U04041	Hs 17548	ESTs
18727	U04041	Hs 17548	ESTs
41381	U04041	Hs 17548	ESTs
23376	U04041	Hs 17548	ESTs
52759	U04041	Hs 17548	ESTs
37690	U04041	Hs 17548	ESTs
40911	U04041	Hs 17548	ESTs
37064	U04041	Hs 17548	ESTs
26355	U04041	Hs 17548	ESTs
2188	U04041	Hs 17548	ESTs
2945	U04041	Hs 17548	ESTs
4297	U04041	Hs 17548	ESTs
8127	U04041	Hs 17548	ESTs
20614	U04041	Hs 17548	ESTs
5822	U04041	Hs 17548	ESTs
4328	U04041	Hs 17548	ESTs
3358	U04041	Hs 17548	ESTs
24545	U04041	Hs 17548	ESTs
33309	U04041	Hs 17548	ESTs





**FIGURE 3 (CONT.)**

[illegible]



**FIGURE 3 (CONT.)**

[illegible]

**FIGURE 3 (CONT.)**

350	AA352645	Hs 141644	ESTs	Human transcription mRNA for TRAF3 complete cds
351	AA352646	Hs 081008	ESTs	
352	AF043128	Hs 20728	ESTs	THROMBOXANE SYNTHASE
353	AF081816	Hs 20116	ESTs	
354	AA253400	Hs 104326	ESTs	
355	AA411144	Hs 104788	ESTs	
356	AA68738	Hs 142920	ESTs	
357	AJ230841	Hs 40129	ESTs	Highly similar to 60S RIBOSOMAL PROTEIN L38 [Rattus norvegicus]
358	U10090	Hs 37100	ESTs	Human MAGE-Sa antigen (MAGE-Sa) gene complete cds
359	AF1003	Hs 107070	ESTs	
360	L1484	Hs 12136	ESTs	Human Rex encoding protein Rlp-1 mRNA complete cds
361	U53766	Hs 54485	ESTs	
362	AF179110	Hs 95952	ESTs	EST - RC_H62196
363	H52296	Hs 30660	EST	
364	L10335	Hs 040726	EST	EST - RC_AA00726
365	AF125725	Hs 96433	ESTs	Human RPLP0 mRNA for RPLP032 gene complete cds
366	AF257210	U7534	ESTs	U7534/16477/RR4411307_JA
367	AF290738	Hs 129078	ESTs	
368	AA338710	Hs 87185	ESTs	H. sapiens RNA in CLCH3
369	HG274737	EST - HG274737	ESTs	
370	AF6208	Hs 35533	ESTs	
371	AA417027	Hs 104787	EST	
372	AA275504	Hs 85629	ESTs	
373	AB8774	Hs 2223	ESTs	Human sapiens mRNA for KIA0293 gene partial cds
374	AA398120	Hs 87564	ESTs	
375	AA332686	Hs 17151	ESTs	
376	AF12925	Hs 100200	ESTs	Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]
377	AF12925	Hs 100200	ESTs	Non-membrane-anchoring protein (NMAP) mRNA complete cds
378	AA468928	Hs 80002	ESTs	ESTs Weakly similar to LCN [H. maculosa]
379	AF28197	Hs 80002	EST	
380	AA487501	Hs 11329	ESTs	
381	AF18777	Hs 23987	EST	
382	AA320837	Hs 22507	ESTs	
383	AF7468	Hs 75996	ESTs	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3
384	AA255681	Hs 20023	ESTs	
385	AA451901	Hs 78537	ESTs	Human actin/thymosin beta mRNA partial cds
386	AA127459	Hs 100785	ESTs	
387	H52683	Hs 124151	ESTs	
388	U51808	Hs 37137	ESTs	Human U2-45a protein U2 mRNA complete cds
389	AA331293	Hs 47319	ESTs	
390	AA454840	Hs 96533	ESTs	
391	AF16459	Hs 30632	ESTs	Human mRNA for KIA02106 gene complete cds
392	H64637	Hs 120777	ESTs	ESTs Weakly similar to ELL [M. musculus]
393	U78718	Hs 12246	EST	Human cdcin (RELN) mRNA complete cds
394	U78718	Hs 12246	EST	EST - YELG10614MSZ1
395	L016CAH4521	Hs 95044	ESTs	
396	AF31353	Hs 431	ESTs	Mouse Islet-1a (Isl-1) oncogene in translog
397	AF970205	EST - RC_AA35610	EST	
398	AA432810	Hs 40389	ESTs	
399	H58331	Hs 86547	ESTs	
400	AF278978	Hs 428991	EST	
401	AF183272	Hs 29417	ESTs	ESTs Weakly similar to CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF4 [H. sapiens]
402	AF104934	Hs 122848	ESTs	
403	AF104934	Hs 122848	ESTs	PROTEIN-TYROSINE PHOSPHATASE 2C
404	AF104934	Hs 122848	ESTs	Human mRNA for KIA0381 gene complete cds
405	AA412024	Hs 104732	ESTs	
406	AF104934	Hs 122848	ESTs	
407	AF104934	Hs 122848	ESTs	
408	AF104934	Hs 122848	ESTs	
409	AF104934	Hs 122848	ESTs	
410	AF104934	Hs 122848	ESTs	
411	AF104934	Hs 122848	ESTs	
412	AF104934	Hs 122848	ESTs	
413	AF104934	Hs 122848	ESTs	
414	AF104934	Hs 122848	ESTs	
415	AF104934	Hs 122848	ESTs	
416	AF104934	Hs 122848	ESTs	
417	AF104934	Hs 122848	ESTs	
418	AF104934	Hs 122848	ESTs	
419	AF104934	Hs 122848	ESTs	
420	AF104934	Hs 122848	ESTs	
421	AF104934	Hs 122848	ESTs	
422	AF104934	Hs 122848	ESTs	
423	AF104934	Hs 122848	ESTs	
424	AF104934	Hs 122848	ESTs	
425	AF104934	Hs 122848	ESTs	

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## FIGURE 3 (CONT.)

42790	10	T8105	Hs.142875	ESTs	
4713	10	Y01864	EST - 106564		
4818	10	X01843	Hs.29117	Human mRNA for per alpha-extended 1-unrestrained region	
3327	10	C27379	Hs.3234	EST	Human mRNA for per alpha-extended 1-unrestrained region
3118	10	C27379	Hs.3234	EST	Human mRNA for per alpha-extended 1-unrestrained region
3018	10	U72449	Hs.5073	EST	
2918	10	A242578	Hs.49107	ESTs	
3158	10	R3117	Hs.100469	Human A1-A mRNA complete cds	
40113	10	H17003	Hs.12596	ESTs	
10201	10	A008235	Hs.8972	ESTs	Human mRNA for probable ubiquitin carboxyl-terminal hydrolase (Hs.11.3) [C. elegans]
37481	10	A033239	Hs.8030	ESTs	Human mRNA for probable ubiquitin carboxyl-terminal hydrolase (Hs.11.3) [C. elegans]
23800	10	T85788	Hs.17869	ESTs	
354	10	D14837	Hs.81882	Human mRNA for KIAA0101 gene complete cds	
6833	10	Z57331	Hs.25055	Ubiquitin-conjugating enzyme E2H (homologous to yeast UBC4)	
29893	10	H97019	Hs.42453	ESTs	
26482	10	A032451	Hs.4722	ESTs	
33123	10	T23306	Hs.13395	EST	
26325	10	A018392	Hs.13395	EST	
11119	10	A018392	Hs.13395	EST	
30432	10	A038184	Hs.6641	EST	Human mRNA for Hsp70 family group protein HMG2s
31152	10	D51891	Hs.82265	Phosphoenolpyruvate carboxykinase (phosphoenolpyruvate synthetase) (Hs.11.3) [C. elegans]	
21152	10	H65043	Hs.13810	ESTs	Human mRNA for Hsp70 family group protein HMG2s
31372	10	R01179	Hs.112536	ESTs	
17903	10	A1102258	Hs.110524	ESTs	
20747	10	H98842	Hs.10333	ESTs	
4878	10	U33206	Hs.79019	Human mRNA for KIAA0101 gene complete cds	
34563	10	A031587	Hs.10001	Human mRNA for KIAA0101 gene complete cds	
30964	10	A027006	Hs.112204	ESTs	
3638	10	U13126	Hs.38573	Human beta-12, N-acetylglucosaminyltransferase II (MGAT2) gene complete cds	
7074	10	D12104	Hs.3350	ESTs	
107	10	A030174	Hs.3350	ESTs	
40113	10	U01700	Hs.131478	Human DP proteinase receptor (PTGDR) mRNA partial cds	
30009	10	A040237	Hs.24453	Human protein calcium channel (Hsp3) mRNA complete cds	
19879	10	U70602	Hs.23442	ESTs	Human mRNA for KIAA0101 gene complete cds
14373	10	H26813	Hs.37628	EST	
17396	10	T40145	Hs.21921	ESTs	
40541	10	A009555	Hs.41175	ESTs	
28496	10	H54534	Hs.101498	ESTs	
29943	10	R62106	Hs.40672	EST	
17997	10	A018833	Hs.42993	ESTs	Human mRNA for KIAA0101 gene complete cds
21320	10	R11073	Hs.12825	EST	
13683	10	A070317	Hs.18927	ESTs	
30539	10	H49072	Hs.34827	ESTs	Human mRNA for KIAA0101 gene complete cds
27778	10	H49072	Hs.34827	ESTs	Human mRNA for KIAA0101 gene complete cds
18490	10	A0337012	Hs.15321	EST	
40812	10	X56532	Hs.88064	EST	
803	10	H83418	Hs.06870	Human A11 mRNA complete cds	
22074	10	D00070	Hs.90	ATL-derived PMA-1-positive (APR) peptide	
40807	10	R87100	Hs.33665	ESTs	
13244	10	N82395	Hs.56593	TRANSCRIPTION INITIATION FACTOR IF BETA SUBUNIT	
32796	10	W00904	Hs.8037	ESTs	
18263	10	R07075	Hs.23074	Zinc finger protein 3, linked	
19682	10	A0326487	Hs.97489	ESTs	
41867	10	H47381	Hs.33947	ESTs	
2548	10	R07886	Hs.87197	CLEAVAGE SIGNAL-1 PROTEIN	
7736	10	A025897	Hs.81564	Protein factor 4	
	10	A0332121	Hs.108531	Human lysophospholipase mRNA complete cds	

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**FIGURE 3 (CONT.)**

Accession	Gene	Protein	Function
AA033524	Ha_111931	EST	
AA033525	Ha_107246	EST	
AA033526	Ha_107245	EST	
AA033527	Ha_107244	EST	
AA033528	Ha_107243	EST	
AA033529	Ha_107242	EST	
AA033530	Ha_107241	EST	
AA033531	Ha_107240	EST	
AA033532	Ha_107239	EST	
AA033533	Ha_107238	EST	
AA033534	Ha_107237	EST	
AA033535	Ha_107236	EST	
AA033536	Ha_107235	EST	
AA033537	Ha_107234	EST	
AA033538	Ha_107233	EST	
AA033539	Ha_107232	EST	
AA033540	Ha_107231	EST	
AA033541	Ha_107230	EST	
AA033542	Ha_107229	EST	
AA033543	Ha_107228	EST	
AA033544	Ha_107227	EST	
AA033545	Ha_107226	EST	
AA033546	Ha_107225	EST	
AA033547	Ha_107224	EST	
AA033548	Ha_107223	EST	
AA033549	Ha_107222	EST	
AA033550	Ha_107221	EST	
AA033551	Ha_107220	EST	
AA033552	Ha_107219	EST	
AA033553	Ha_107218	EST	
AA033554	Ha_107217	EST	
AA033555	Ha_107216	EST	
AA033556	Ha_107215	EST	
AA033557	Ha_107214	EST	
AA033558	Ha_107213	EST	
AA033559	Ha_107212	EST	
AA033560	Ha_107211	EST	
AA033561	Ha_107210	EST	
AA033562	Ha_107209	EST	
AA033563	Ha_107208	EST	
AA033564	Ha_107207	EST	
AA033565	Ha_107206	EST	
AA033566	Ha_107205	EST	
AA033567	Ha_107204	EST	
AA033568	Ha_107203	EST	
AA033569	Ha_107202	EST	
AA033570	Ha_107201	EST	
AA033571	Ha_107200	EST	
AA033572	Ha_107199	EST	
AA033573	Ha_107198	EST	
AA033574	Ha_107197	EST	
AA033575	Ha_107196	EST	
AA033576	Ha_107195	EST	
AA033577	Ha_107194	EST	
AA033578	Ha_107193	EST	
AA033579	Ha_107192	EST	
AA033580	Ha_107191	EST	
AA033581	Ha_107190	EST	
AA033582	Ha_107189	EST	
AA033583	Ha_107188	EST	
AA033584	Ha_107187	EST	
AA033585	Ha_107186	EST	
AA033586	Ha_107185	EST	
AA033587	Ha_107184	EST	
AA033588	Ha_107183	EST	
AA033589	Ha_107182	EST	
AA033590	Ha_107181	EST	
AA033591	Ha_107180	EST	
AA033592	Ha_107179	EST	
AA033593	Ha_107178	EST	
AA033594	Ha_107177	EST	
AA033595	Ha_107176	EST	
AA033596	Ha_107175	EST	
AA033597	Ha_107174	EST	
AA033598	Ha_107173	EST	
AA033599	Ha_107172	EST	
AA033600	Ha_107171	EST	
AA033601	Ha_107170	EST	
AA033602	Ha_107169	EST	
AA033603	Ha_107168	EST	
AA033604	Ha_107167	EST	
AA033605	Ha_107166	EST	
AA033606	Ha_107165	EST	
AA033607	Ha_107164	EST	
AA033608	Ha_107163	EST	
AA033609	Ha_107162	EST	
AA033610	Ha_107161	EST	
AA033611	Ha_107160	EST	

## FIGURE 3 (CONT.)

26294	AA12154	Hs 88415	EST4	
10864	AA12153	Hs 88415	EST4	
16914	AA12152	Hs 88415	EST4	
35907	AA12151	Hs 88415	EST4	
21672	AA12150	Hs 88415	EST4	
19916	AA12149	Hs 88415	EST4	
10511	AA12148	Hs 88415	EST4	
17721	AA12147	Hs 88415	EST4	
42302	AA12146	Hs 88415	EST4	
28134	AA12145	Hs 88415	EST4	
18766	AA12144	Hs 88415	EST4	
34482	AA12143	Hs 88415	EST4	
23975	AA12142	Hs 88415	EST4	
29842	AA12141	Hs 88415	EST4	
35389	AA12140	Hs 88415	EST4	
35398	AA12139	Hs 88415	EST4	
5793	AA12138	Hs 88415	EST4	
19978	AA12137	Hs 88415	EST4	
1280	AA12136	Hs 88415	EST4	
21971	AA12135	Hs 88415	EST4	
23765	AA12134	Hs 88415	EST4	
35123	AA12133	Hs 88415	EST4	
38232	AA12132	Hs 88415	EST4	
35216	AA12131	Hs 88415	EST4	
29418	AA12130	Hs 88415	EST4	
4834	AA12129	Hs 88415	EST4	
42504	AA12128	Hs 88415	EST4	
8111	AA12127	Hs 88415	EST4	
7173	AA12126	Hs 88415	EST4	
99	AA12125	Hs 88415	EST4	
28109	AA12124	Hs 88415	EST4	
888	AA12123	Hs 88415	EST4	
28848	AA12122	Hs 88415	EST4	
30828	AA12121	Hs 88415	EST4	
22567	AA12120	Hs 88415	EST4	
9347	AA12119	Hs 88415	EST4	
11896	AA12118	Hs 88415	EST4	
40584	AA12117	Hs 88415	EST4	
193	AA12116	Hs 88415	EST4	
18305	AA12115	Hs 88415	EST4	
6078	AA12114	Hs 88415	EST4	
28741	AA12113	Hs 88415	EST4	
35869	AA12112	Hs 88415	EST4	
23804	AA12111	Hs 88415	EST4	
40583	AA12110	Hs 88415	EST4	
31428	AA12109	Hs 88415	EST4	
8169	AA12108	Hs 88415	EST4	
39524	AA12107	Hs 88415	EST4	
34578	AA12106	Hs 88415	EST4	
38078	AA12105	Hs 88415	EST4	
23926	AA12104	Hs 88415	EST4	
9226	AA12103	Hs 88415	EST4	
18146	AA12102	Hs 88415	EST4	
18185	AA12101	Hs 88415	EST4	
21228	AA12100	Hs 88415	EST4	
41283	AA12099	Hs 88415	EST4	
24911	AA12098	Hs 88415	EST4	
1566	AA12097	Hs 88415	EST4	

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## FIGURE 3 (CONT.)

20550	58	MS2013	Hs.24100	ESTs	
28470	59	AA25179	Hs.10470	ESTs	
16574	59	AA03170	Hs.13960	EST	
495	59	D2007	Hs.45028	Human mRNA for KIAA0195 gene partial cds	
4023	59	U23162	Hs.82383	Human nucleoside triphosphate ADE37.2 mRNA complete cds	
1192	58	G35566-H73744	EST - HQ3546-H73744	EST	
27856	58	T10248	Hs.4280	ESTs	
30723	58	AA43524	Hs.97483	EST	
1114	58	L40384	Hs.109270	EST - L40384	
28872	58	AA491137	EST - J08206_cds2	ESTs	
4705	58	Z05871	Hs.14090	ESTs	
29173	58	C21118	Hs.8444	ESTs	
10290	58	AA211901	Hs.86429	ESTs	
732	58	D81381	Hs.22559	Human mRNA for KIAA0197 gene partial cds	
5330	58	U91327	EST - U91327	EST	
33503	58	V63710	Hs.35196	EST	
2553	58	M20107	Hs.72933	Human protein (accession 4 version 1) (PF11617) gene complete cds	
34703	58	AA293807	Hs.95952	ESTs Weakly similar to putative p150 [H.sapiens]	
42655	58	V97859	Hs.108932	ESTs	
33160	58	AA487465	EST - RC_AA487465	EST	
4244	57	U33236	Hs.90073	Human chromosome 1 integration gene homolog CAS mRNA complete cds	
32822	57	V16534	Hs.53378	ESTs	
24673	57	Z38201	Hs.7859	ESTs	
9216	57	U18991	Hs.2516	STR (recombinant region 7) box 9 (chromosome 12) gene partial cds	
30726	57	Z68529	Hs.139603	ESTs	
30726	57	AA203231	Hs.173283	Human mRNA for KIAA0229 gene partial cds	
11409	57	AA203231	Hs.173283	ESTs	
22538	57	R23487	Hs.4520	Human coding region mRNA-L, precursor (A04442) mRNA complete cds	
49747	57	N75994	Hs.11175	Human alpha-actinin 2 mRNA, alternative splice variant alpha-1 complete cds	
31596	57	X82279	Hs.43234	EST - X82279	
31578	56	N71361	Hs.50019	ESTs	
33207	56	V70051	Hs.66178	Human mRNA for M-phase phosphoprotein myp3	
7545	56	M25753	Hs.23960	Cyclin B1	
22500	56	R78156	Hs.29613	ESTs	
33582	56	V69127	Hs.59422	ESTs	
28463	56	C02522	Hs.113618	ESTs	
37867	56	V71784	Hs.89099	CCD1 HOMOLOG	
44185	56	AA203231	Hs.173283	ESTs	
4732	55	V72118	Hs.104333	Human coding region clone Z0222 mRNA sequence	
3299	55	U58522	Hs.64713	Human histidine-interacting protein (HIF2) mRNA complete cds	
28720	55	AA396574	Hs.65370	ESTs	
746	55	D84454	Hs.21699	Human mRNA for UDP-glucose 6-epimerase complete cds	
29573	55	C21517	Hs.63313	ESTs	
3117	54	M81182	Hs.76781	Pericardial membrane protein 1 (PMO Zellweger syndrome)	
21297	54	R09186	Hs.20321	ESTs Moderately similar to M-phase phosphoprotein 11 [H.sapiens]	
31447	54	N69507	Hs.129849	ESTs	
28794	54	F03153	Hs.80383	ESTs	
38928	54	AA009383	Hs.109960	ESTs	
29603	54	N23368	Hs.83864	EST	
30925	53	N52795	Hs.144393	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]	
32025	53	H07864	Hs.27734	ESTs	
28200	53	AA141620	Hs.34990	EST - AA141620	
9470	53	H04817	EST - H04817	EST	
8435	53	H02021	EST - H02021	EST	
28557	53	C20914	Hs.84497	ESTs	
27411	53	AA128137	Hs.86434	ESTs	

## FIGURE 3 (CONT.)

30615	53	N02556	Hs 47078	ESTs	
30616	53	AA399209	Hs 80058	ESTs	
30617	53	C00622	Hs 7872	ESTs	
30618	53	N24194	Hs 41331	ESTs	
30619	53	G3446-AT2783	EST - HG1845-AT7643		
30620	53	F08925	Hs 49510	ESTs	
30621	53	AA100304	Hs 25710	ESTs	ESTs weakly similar to unknown (S. cerevisiae)
30622	53	M12139	Hs 2421	ESTs	Human small protein rich protein (SPR1) mRNA clone 122
30623	53	AA37150	Hs 8384	ESTs	
30624	53	AA37151	Hs 8384	ESTs	ESTs weakly similar to SPERMATID SPECIFIC PROTEIN 12 (Scsa offshoot)
30625	53	AA37152	Hs 4206	ESTs	EST - AA325118
30626	53	N02593	Hs 12670	ESTs	ESTs weakly similar to weak similarity to procollagen alpha chain (V) chain (C. elegans)
30627	53	AA37153	Hs 10418	ESTs	
30628	53	AA37154	Hs 38389	ESTs	ESTs weakly similar to ROSA26AS (M. musculus)
30629	53	AA37155	Hs 22164	ESTs	
30630	53	Z18810	Hs 27184	ESTs	
30631	53	C11245	Hs 11171	ESTs	H. sapiens mRNA for apoptosis specific protein
30632	53	X17098	Hs 108318	ESTs	Pregnancy-specific beta-1 glycoprotein B
30633	53	N31781	Hs 47338	ESTs	
30634	53	AA37156	Hs 88028	ESTs	
30635	53	AA37157	Hs 44810	ESTs	
30636	53	M15796	Hs 78998	ESTs	Proliferating cell nuclear antigen
30637	53	N02595	Hs 44950	ESTs	Human sapiens clone 24739 mRNA sequence
30638	53	AA37158	Hs 10205	ESTs	
30639	53	AA37159	Hs 11358	ESTs	
30640	53	AA37160	Hs 11358	ESTs	
30641	53	T79651	Hs 11358	ESTs	
30642	53	F08134	Hs 12839	ESTs	
30643	53	AA37161	Hs 85003	ESTs	
30644	53	AA37162	Hs 87329	ESTs	
30645	53	AA37163	Hs 84330	ESTs	
30646	53	AA37164	Hs 86178	ESTs	H. sapiens mRNA for M-phase phosphoprotein mepp
30647	53	AA37165	Hs 12544	ESTs	
30648	53	AA37166	Hs 42978	ESTs	
30649	53	AA37167	Hs 32178	ESTs	ESTs weakly similar to MOESIN/ZENKIN/CAKIN HOMOLOG (D. melanogaster)
30650	53	U36764	Hs 87998	ESTs	Eukaryotic translation initiation factor 3 (eIF-3) subunit
30651	53	N02596	Hs 11158	ESTs	Human sapiens mRNA for KIAA0358 protein complete cds
30652	53	AA37168	Hs 5101	ESTs	Human sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
30653	53	N02597	Hs 42478	ESTs	
30654	53	N02598	Hs 22970	ESTs	
30655	53	AA481218	EST - AA481218		
30656	53	AA37169	Hs 27821	ESTs	Human sapiens vsmgphom F homolog mRNA complete cds
30657	53	U15128	Hs 36573	ESTs	Human beta-12, N-acetylglucosaminyltransferase II (MGAT2) gene complete cds
30658	53	AA004420	Hs 49360	ESTs	
30659	53	V707014	Hs 103163	ESTs	
30660	53	AA267833	Hs 89808	ESTs	
30661	53	AA267837	Hs 20137	ESTs	
30662	53	T40289	Hs 6579	ESTs	
30663	53	N02599	Hs 100784	ESTs	Human sapiens mRNA for KIAA0584 protein partial cds
30664	53	V07006	Hs 79440	ESTs	Human sapiens putative RNA binding protein KDC (KDC) mRNA complete cds
30665	53	AA37170	Hs 101618	ESTs	
30666	53	AA37171	Hs 71129	ESTs	
30667	53	AA481219	Hs 92110	ESTs	
30668	53	N02600	Hs 4334	ESTs	
30669	53	AA271803	Hs 41137	ESTs	ESTs weakly similar to synaptonemal complex protein sept-1 (D. melanogaster)
30670	53	R27183	Hs 141123	ESTs	ESTs highly similar to GTP-BINDING PROTEIN LEPA (Pseudomonas fluorescens)
30671	53	H11780	Hs 23606	ESTs	
30672	53	N02601	Hs 84181	ESTs	
30673	53	N02602	Hs 84181	ESTs	
30674	53	N02603	Hs 84181	ESTs	

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## FIGURE 3 (CONT.)

2467	23106	Hs 27785	EST	
2468	Hs6015	Hs 48232	EST	
2469	GUH141107	Hs41515	EST	
1108	GUH141137	EST	Hs41515	
18712	A148106	Hs 46076	EST	
34667	A231156	Hs 40323	EST	Human sapiens spleen reticulin chaperonin BUB3 (BUB3) mRNA complete cds
34762	A231156	Hs 85504	EST	
11935	A231734	Hs 102909	EST	
4295	A242819	Hs 32539	EST	
17822	A405582	Hs 125014	EST	
33781	A1131584	Hs 71435	EST	ESTs Weakly similar to GCF 1 PROTEIN [Saccharomyces cerevisiae]
34754	A1131584	Hs 95187	EST	
33237	A3387642	Hs 81846	EST	Human mRNA for LOC40078 gene complete cds
37667	T47251	Hs 86010	EST	
11588	A400318	Hs 110105	EST	ESTs Highly similar to GOS RIBOSOMAL PROTEIN L26 [Rattus norvegicus]
36222	A428786	Hs 26078	EST	
36223	A428786	Hs 141882	EST	
36224	A428786	Hs 141882	EST	
36225	A428786	Hs 141882	EST	
18208	A115507	Hs 21503	EST	Chondrogenesis 2-oxyltransferase (E2 component of pyruvate dehydrogenase complex)
32718	T11045	Hs 30303	EST	Chondrogenesis 2-oxyltransferase (E2 component of pyruvate dehydrogenase complex)
32719	Hs4355	Hs 54499	EST	Colony type 1 alpha-2
6698	L33951	Hs 69550	EST	SODIUM CHANNEL PROTEIN BRAIN 9 ALPHA SUBUNIT
35400	A339591	Hs 97851	EST	Integrin transmembrane protein 1
35246	A339591	Hs 97851	EST	Human sapiens putative DNA methyltransferase (DNMT2) mRNA complete cds
36337	A428270	Hs 86498	EST	ESTs Weakly similar to HSP90 protein [M. musculus]
21500	R27314	Hs 23620	EST	
31381	Hs7888	Hs 49397	EST	
26725	A428781	Hs 93321	EST	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP25 [Saccharomyces cerevisiae]
17408	A428781	Hs 79310	EST	Human GTP SRT binding protein mRNA complete cds
4908	U07156	Hs 81458	EST	EST - NC_011113
30284	Hs4967	Hs 48624	EST	Human (chondrogenesis) kinase kinase kinase 5 (MAP3K5) mRNA complete cds
30286	A448947	Hs 117018	EST	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOGY [Nucleobius concavus]
13073	A443360	Hs 23530	EST	
40413	R21814	Hs 100358	EST	Human sapiens basic leucine zipper transcription factor MafK (MAF) mRNA complete cds
14474	A4500427	Hs 24164	EST	ESTs Moderately similar to Hs 111380
38213	A448847	Hs 111380	EST	ESTs Weakly similar to Hs 111380
5312	U06716	Hs 79187	EST	Human cell surface protein HCAR mRNA complete cds
24225	W03326	Hs 18500	EST	
35588	A401750	Hs 87243	EST	
29729	Hs9626	Hs 42710	EST	
7203	A403206	Hs 27710	EST	EST - A403206
2157	L41839	Hs 69403	EST	Human sapiens protein tyrosine kinase EPHB2 (EPHB2) mRNA complete cds
3803	A115110	Hs 23054	EST	ESTs Weakly similar to Hs 23054
3804	A115110	Hs 23054	EST	ESTs Weakly similar to Hs 23054
774	D15453	Hs 77985	EST	Human sapiens DNA polymerase gamma
34006	A4188161	Hs 50583	EST	
32658	W05477	Hs 111160	EST	ESTs Weakly similar to Hs 111160
34005	A4185517	Hs 90011	EST	Adenylyltransferase synthase
6028	X04503	Hs 108102	EST	Cyclonema B561
4186	U79463	Hs 108102	EST	
40762	Hs1582	Hs 108102	EST	
22687	R52708	Hs 34161	EST	
41069	Hs3969	Hs 81107	EST	Human sapiens mRNA for Hs 81107
8264	A401334	Hs 100941	EST	
27588	A443187	Hs 41181	EST	
25882	A4412647	Hs 122578	EST	
11016	A403080	Hs 110126	EST	Human bannin-like sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
15921	T12005	Hs 5032	EST	Human sapiens mRNA for nuclear protein thapsig

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## FIGURE 3 (CONT.)

13236	AA63342	Hs.31045	ESTs	
25565	AA112288	Hs.10782	ESTs	
34018	AA191488	Hs.75614	Human high-affinity copper uptake protein (CTR1) mRNA complete cds	
251	D14520	Hs.14726	Basic transcription element binding protein 2	
3778	U09648	Hs.363	Zinc finger protein 139 (clone p12-37)	
24315	Z38409	Hs.8053	ESTs	
16338	AA353738	Hs.8958	Human mRNA for KIAA0118 gene partial cds	
34043	AA353738	Hs.8958	ESTs	
26483	AA432208	Hs.10410	ESTs	
26148	AA432208	Hs.10410	ESTs	
41001	U02536	Hs.3260	ESTs	
41009	Hs.3749	ESTs	ESTs	
5600	X16396	Hs.37791	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE	
19704	Hs.1828	Hs.26390	ESTs	
42223	T98152	Hs.79432	Forkhead 2	
25928	AA342560	Hs.47232	ESTs	
25487	Hs.2565	Hs.36055	ESTs	
19726	Hs.12453	Hs.13026	ESTs	
36267	AA424046	Hs.88305	ESTs	
32237	R34728	Hs.89483	ONAPREPAIR PROTEIN (RCC1)	
17365	AA101531	Hs.68900	ESTs	
13496	Hs.3260	ESTs	ESTs	
13126	AA134904	Hs.44141	ESTs	
40332	Hs.7545	Hs.10806	Human asplasma mRNA from chromosome 5q21.22 clone A3-A	
7719	AA205119	Hs.79326	Human asplasma protein phosphatase 2A B56-epsilon (PPP2A) mRNA complete cds	
10006	N11193	Hs.43132	Human asplasma mRNA for KIAA0028 protein complete cds	
32865	AA181560	Hs.81890	Human asplasma protein base subunit mRNA complete cds	
9570	Hs.65183	Hs.24837	Human asplasma sodium/myo-inositol cotransporter (SLC5A3) gene complete cds	
37551	AA458679	Hs.72356	ESTs	
896	D08613	Hs.28246	Human mRNA for HCC1A complete cds	
23050	T09293	Hs.18144	ESTs	
19367	AA24180	Hs.32332	ESTs	
42494	Hs.32332	ESTs	ESTs	
14310	AA396412	Hs.100002	Hs.100002 Human ribulose 1,5-bisphosphate carboxylase/oxygenase (rbcL) gene (clone 133)	
18233	Hs.8179	ESTs	ESTs	
12253	Hs.8179	ESTs	ESTs	
36165	AA421409	Hs.31838	ESTs	
21555	R35013	Hs.24395	ESTs	
13707	AA463234	Hs.11837	ESTs	
4726	U05786	Hs.75301	Human FX protein mRNA complete cds	
7256	AA075427	Hs.17296	ESTs	
17041	AA070264	Hs.17296	ESTs	
15504	W02362	Hs.44131	ESTs	
23793	T09271	Hs.44131	ESTs	
18214	AA189633	Hs.86091	ESTs	
1401	AA094600	Hs.55632	Human transcription initiation factor eIF3 p69 subunit mRNA complete cds	
18912	F10013	Hs.12415	Human segment clone 23817 unknown mRNA, partial cds	
36317	AA425069	Hs.57272	Human mRNA for KIAA0334 gene complete cds	
9410	Hs.31746	ESTs	ESTs	
2146	Hs.31746	ESTs	ESTs	
11406	Hs.36154	ESTs	ESTs	
33881	Hs.36154	ESTs	ESTs	
14435	AA090120	Hs.4192	ESTs	
6584	Hs.8128	Hs.41127	ESTs	
22061	AA110223	Hs.21984	ESTs	
33786	AA110223	ESTs	ESTs	
37403	Hs.128708	ESTs	ESTs	
15786	X18889	Hs.80009	ALPHA-GALACTOSIDASE A PRECURSOR	
15840	X17044	Hs.91379	PTB-ASSOCIATED SPLICING FACTOR	



## FIGURE 3 (CONT.)

19050	10	HO5509	Hs.24539	EST1	
20530	30	AA278650	Hs.32781	EST1	
18806	30	AA232358	Hs.11921	Human sapiens mRNA for KIAA0418 protein partial cds	
29088	30	F13700	Hs.115623	Human sapiens ribonuclease P protein subunit p10 (RPP40) gene complete cds	
22960	30	U10272	Hs.4287	EST1	
33315	30	W93000	Hs.69389	EST1	
220	30	D13627	Hs.84021	Human mRNA for KIAA0022 gene complete cds	
4798	30	U36416	Hs.74574	Human Cx27-dependent activator protein for secretion mRNA complete cds	
4443	30	AA100828	Hs.100948	EST1	
40615	30	AA100828	Hs.100948	EST1	
18015	30	AA178337	Hs.73396	EST1	
7782	30	AA283339	Hs.130761	EST1	
9948	30	HO5668	Hs.112013	EST1	
505	30	D37009	Hs.43834	Human (Homo) DNA for immunoglobulin light chain	
36417	30	AA504255	Hs.54404	Human protein kinase ATR mRNA complete cds	
41664	30	R46337	Hs.107450	EST1	
9002	30	L18161	Hs.121541	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT	
16976	30	AA053625	Hs.60690	EST1	
37426	30	AA454018	Hs.69308	EST1	
2358	30	W77878	Hs.8450	Zinc finger protein 84 (ZFP84)	
15174	30	U29287	Hs.87248	Human Bcl-2 binding component 2 (Bcl2) mRNA partial cds	
33870	30	W93343	Hs.59509	EST1	
6794	30	Y11861	Hs.9904	Human sapiens ribosomal protein S17 gene nuclear gene encoding mitochondrial protein complete cds	
41077	30	NP5028	Hs.125031	EST1	
1932	30	U14894	Hs.73039	Human (Homo) mRNA complete cds	
16106	30	AA202359	Hs.69603	EST1	
32134	30	R40351	Hs.42863	EST1	
12617	30	AA455648	Hs.20661	EST1	
11989	30	AA281251	Hs.35095	EST1 Weakly similar to ribonuclease protein end (D melanogaster)	
6028	30	Z68184	Hs.60619	Phosphatase domain hemoglobin-like HeLaCat mRNA 2106 nt	
15446	30	W27374	Hs.5300	Human sapiens (Homo) protein (BC10) mRNA complete cds	
33066	30	AA482357	Hs.05138	EST1	
13878	30	AA478604	Hs.7114	EST1	
6209	30	X18770	Hs.49007	Human PAP mRNA	
388	30	D37871	Hs.51	Phosphatidylserine glycan class A (patent) and nucleolar hemoglobin	
1311	30	G175-H75203	Hs.10122	EST1	
42614	30	W37604	Hs.10122	EST1	
29115	30	AA201872	Hs.39188	EST1	
29115	30	AA201872	Hs.39188	EST1	
29115	30	AA201872	Hs.39188	EST1	
4083	30	U96815	Hs.85613	Human SV40NSF complex 125 kDa subunit (BAF 125) mRNA complete cds	
10194	30	R23855	Hs.107598	EST1	
15039	30	U48116	Hs.89027	Protein tyrosine phosphatase receptor type gamma polypeptide	
1005	30	L00038	Hs.79070	V-myc avian myeloblastosis viral oncogene homolog	
4336	30	U48705	Hs.75592	Receptor protein-tyrosine kinase EDDR1	
10173	30	R30878	Hs.102992	EST1 Weakly similar to cell division control protein COC1 (H. sapiens)	
26355	30	AA278071	Hs.84445	EST1 Weakly similar to TDA11.2 (C. elegans)	
4401	30	U41515	Hs.85318	Human deleted in spleen lymphoma 1 (DIS1) mRNA complete cds	
21009	30	NP0401	Hs.28928	EST1	
3602	30	U01317	Hs.117944	HEMOGLOBIN EPSILON CHAIN	
4833	30	U53455	Hs.34470	Sulfonylurea receptor (hypothalamic)	
36200	30	AA421164	Hs.107213	EST1	
26443	30	AA210708	Hs.107221	EST1	
10099	30	AA15558	Hs.122803	Human factor beta-1 (prothrombin) transcription factor 1-like	
5210	30	U53440	Hs.82819	Human CUL-2 (cag-2) mRNA complete cds	
12313	30	AA297818	Hs.22585	EST1	
3928	30	AA20248	Hs.73186	WEE1-LIKE PROTEIN KIAH6	
39690	30	F09155	Hs.77822	EST1	

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## FIGURE 3 (CONT.)

34	AA321690	Hs 59876	EST
35	AA183318	Hs 62911	ESTs
36	AA183318	Hs 15941	ESTs
37	AA183318	Hs 15941	ESTs
38	AA183318	Hs 15941	ESTs
39	AA183318	Hs 15941	ESTs
40	AA183318	Hs 15941	ESTs
41	AA183318	Hs 15941	ESTs
42	AA183318	Hs 15941	ESTs
43	AA183318	Hs 15941	ESTs
44	AA183318	Hs 15941	ESTs
45	AA183318	Hs 15941	ESTs
46	AA183318	Hs 15941	ESTs
47	AA183318	Hs 15941	ESTs
48	AA183318	Hs 15941	ESTs
49	AA183318	Hs 15941	ESTs
50	AA183318	Hs 15941	ESTs
51	AA183318	Hs 15941	ESTs
52	AA183318	Hs 15941	ESTs
53	AA183318	Hs 15941	ESTs
54	AA183318	Hs 15941	ESTs
55	AA183318	Hs 15941	ESTs
56	AA183318	Hs 15941	ESTs
57	AA183318	Hs 15941	ESTs
58	AA183318	Hs 15941	ESTs
59	AA183318	Hs 15941	ESTs
60	AA183318	Hs 15941	ESTs
61	AA183318	Hs 15941	ESTs
62	AA183318	Hs 15941	ESTs
63	AA183318	Hs 15941	ESTs
64	AA183318	Hs 15941	ESTs
65	AA183318	Hs 15941	ESTs
66	AA183318	Hs 15941	ESTs
67	AA183318	Hs 15941	ESTs
68	AA183318	Hs 15941	ESTs
69	AA183318	Hs 15941	ESTs
70	AA183318	Hs 15941	ESTs
71	AA183318	Hs 15941	ESTs
72	AA183318	Hs 15941	ESTs
73	AA183318	Hs 15941	ESTs
74	AA183318	Hs 15941	ESTs
75	AA183318	Hs 15941	ESTs
76	AA183318	Hs 15941	ESTs
77	AA183318	Hs 15941	ESTs
78	AA183318	Hs 15941	ESTs
79	AA183318	Hs 15941	ESTs
80	AA183318	Hs 15941	ESTs
81	AA183318	Hs 15941	ESTs
82	AA183318	Hs 15941	ESTs
83	AA183318	Hs 15941	ESTs
84	AA183318	Hs 15941	ESTs
85	AA183318	Hs 15941	ESTs
86	AA183318	Hs 15941	ESTs
87	AA183318	Hs 15941	ESTs
88	AA183318	Hs 15941	ESTs
89	AA183318	Hs 15941	ESTs
90	AA183318	Hs 15941	ESTs
91	AA183318	Hs 15941	ESTs
92	AA183318	Hs 15941	ESTs
93	AA183318	Hs 15941	ESTs
94	AA183318	Hs 15941	ESTs
95	AA183318	Hs 15941	ESTs
96	AA183318	Hs 15941	ESTs
97	AA183318	Hs 15941	ESTs
98	AA183318	Hs 15941	ESTs
99	AA183318	Hs 15941	ESTs
100	AA183318	Hs 15941	ESTs

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## FIGURE 3 (CONT.)

17642	27	A1129983	Hs 44155	ESTs	Moderately similar to C-11-TRANSYHDROXYLATE SYNTHASE CYTOPLASMIC [H. sapiens]
4131	27	X72841	Hs 2758	ESTs	Human ribonucleoside-binding protein (RBA48) mRNA complete cds
17653	27	A0732915	Hs 10152	ESTs	EST - RC_A0732915
3403	27	A0232920	Hs 149180	ESTs	ESTs
5183	27	T10065	Hs 4914	ESTs	ESTs
22937	27	U81310	Hs 118910	ESTs	Human telomere TTAGGG repeat TAAAG mRNA complete cds
20037	27	H54116	Hs 47870	ESTs	Human tumor necrosis factor receptor (TNFR) mRNA complete cds
16243	27	A012902	Hs 60256	ESTs	ESTs
18954	27	H89100	Hs 33977	ESTs	ESTs
6444	27	X87750	Hs 90077	ESTs	Human telomere TTAGGG repeat TAAAG mRNA complete cds
5916	27	X81072	Hs 99998	ESTs	Human telomere TTAGGG repeat TAAAG mRNA complete cds
8240	27	X78877	Hs 75066	ESTs	Human telomere TTAGGG repeat TAAAG mRNA complete cds
42116	27	T69224	Hs 97101	ESTs	EST - RC_T09924
7701	27	A0215333	Hs 22347	ESTs	ESTs
17566	27	A012805	Hs 99407	ESTs	Human telomere TTAGGG repeat TAAAG mRNA complete cds
42334	27	X72109	Hs 49448	ESTs	ESTs
24513	27	N71111	Hs 82053	ESTs	ESTs
10208	27	A039458	Hs 10208	ESTs	ESTs
10108	27	S56441	Hs 21103	ESTs	ESTs
32901	27	V03306	Hs 77183	ESTs	Human telomere TTAGGG repeat TAAAG mRNA complete cds
35173	27	A038507	Hs 87181	ESTs	ESTs
10180	27	R60100	Hs 22596	ESTs	ESTs
32563	27	T21897	Hs 21605	ESTs	Human telomere TTAGGG repeat TAAAG mRNA complete cds
34103	27	A028278	Hs 7323	ESTs	ESTs
13223	27	A443720	Hs 7551	ESTs	ESTs
6494	27	A443460	Hs 2430	ESTs	ESTs
7778	27	A028771	Hs 101368	ESTs	ESTs
11605	27	A007124	Hs 30386	ESTs	EST - HC3132-AT3206
3370	27	G03073306	Hs 619	ESTs	Human telomere TTAGGG repeat TAAAG mRNA complete cds
18000	27	F18037	Hs 65371	ESTs	Human telomere TTAGGG repeat TAAAG mRNA complete cds
34780	27	A0291258	Hs 87101	ESTs	ESTs
41955	27	T32311	Hs 1904	ESTs	Neurofilament protein II
2009	27	L32831	Hs 9768	ESTs	ESTs
33608	27	Z33501	Hs 9768	ESTs	EST - HC384-AT84
1385	27	G84-AT84	Hs 27596	ESTs	ESTs
24758	27	A017484	Hs 60668	ESTs	Human telomere TTAGGG repeat TAAAG mRNA complete cds
7620	27	H52078	Hs 13604	ESTs	Human telomere TTAGGG repeat TAAAG mRNA complete cds
20333	27	R29166	Hs 80013	ESTs	Human telomere TTAGGG repeat TAAAG mRNA complete cds
21256	27	N29325	Hs 107914	ESTs	Human telomere TTAGGG repeat TAAAG mRNA complete cds
40228	27	A005883	Hs 77119	ESTs	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE
21823	27	D82775	Hs 10724	ESTs	ESTs
1798	27	A021718	Hs 20120	ESTs	ESTs
3219	27	A041158	Hs 18183	ESTs	ESTs
38197	27	M42712	Hs 18183	ESTs	ESTs
3184	27	A023284	Hs 109822	ESTs	ESTs
7183	27	L33808	Hs 1085	ESTs	ESTs
1033	27	Z11840	Hs 6572	ESTs	ESTs
24908	27	M15983	Hs 87721	ESTs	ESTs
30407	27	A021778	Hs 97721	ESTs	ESTs
24728	27	N48787	Hs 20378	ESTs	ESTs
25008	27	A031206	Hs 72071	ESTs	ESTs
7158	27	A023351	Hs 44339	ESTs	ESTs
26290	27	H58604	Hs 37573	ESTs	ESTs
18922	27	A039418	Hs 23170	ESTs	ESTs
12278	27	R89227	Hs 24005	ESTs	ESTs
22048	27	W52015	Hs 34620	ESTs	ESTs
2101	27				

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## FIGURE 3 (CONT.)

9558	28	Hs1487	Hs12053	EST1	
18104	28	A418801	Hs8534	EST1	
24882	28	Z11553	Hs29375	EST1	
42038	28	Hs8445	Hs4235	EST1	
4865	28	A802259	Hs105478	Human mRNA for KIAA0361 gene KIAA0361 protein	
21148	28	R31831	Hs25828	EST1	
4827	28	U51890	Hs81178	Human hPip18 mRNA complete cds	
8394	28	A4428156	Hs47714	EST1	
20472	28	Hs24906	Hs24906	EST1	
41027	28	R87258	Hs32715	EST1 Moderately similar to nuclein [M. musculus]	
612	28	D83480	Hs74870	Human mRNA for KIAA0146 gene partial cds	
1121	28	U62598	Hs73551	Human mRNA for KIAA0146 gene partial cds	
18207	28	A4428156	Hs32715	EST1 Human proteinase M1 mRNA complete cds	
15368	28	W02596	Hs32715	EST1 Moderately similar to Hs3 [R. norvegicus]	
38023	28	A4428156	Hs32715	EST1 Moderately similar to Hs3 [R. norvegicus]	
38023	28	Hs1574	Hs1574	EST1 Highly similar to HYPOTHETICAL 103.6 KD PROTEIN IN COL53BP1/2 INTERGENIC REGION [Saccharomyces cerevisiae]	
38023	28	A4128719	Hs2282	EST1	
10951	28	474282	Hs81058	RETINOBLASTOMA BINDING PROTEIN P48	
6150	28	C12945	Hs10817	EST1 Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12/ORC5 INTERGENIC REGION [Saccharomyces cerevisiae]	
17793	28	A4150242	Hs71587	EST1 Highly similar to modulator recognition factor 2 [M. musculus]	
29336	28	A4272556	Hs83657	EST1	
29336	28	L47821	Hs83657	EST1	
29336	28	A405149	Hs110103	Human Chromosome 18 BAC clone C181875K-A27021	
29336	28	U41815	Hs81161	Human C-1 mRNA complete cds	
10042	28	A4215298	Hs70830	Human sapiens chromosome 18 contig R30783	
7699	28	X83654	Hs137743	Human sapiens mRNA for SCP-1 complete cds	
6943	28	H87122	Hs82313	EST1	
20538	28	A4428156	Hs82313	EST1	
20538	28	A4428156	Hs82313	EST1	
42906	28	Q71204	Hs111709	Human endonuclease (hucn-1) mRNA complete cds	
38015	28	A4538388	Hs32771	EST1	
11819	28	A4538388	Hs32771	EST1	
37432	28	A454103	Hs110031	EST1	
28270	28	A4531180	Hs84317	EST1	
5587	28	X17482	Hs65506	U7 SMALL NUCLEAR RIBONUCLEOPROTEIN A	
18641	28	H58817	Hs5189	EST1 Highly similar to URQUHART-CONJUGATING ENZYME E2.17 KD [Drosophila melanogaster]	
10053	28	A4040882	Hs10290	EST1	
14053	28	A4435147	Hs12763	EST1 Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R35D3.2 IN CHROMOSOME III [Carcinohabditis elegans]	
31374	28	H71303	Hs50015	EST1	
7614	28	A4192578	Hs102596	EST1 Weakly similar to Yak07Cuep [S. cerevisiae]	
31371	28	A4478195	Hs105020	EST1	
7090	28	A4029913	Hs103360	Human sapiens dephosphorylase protein-2 (DPH2) mRNA complete cds	
24218	28	A4538388	Hs3443	EST1	
24218	28	A4538388	Hs3443	EST1	
18010	28	H03370	Hs132403	Human clone 23900 mRNA sequence	
17119	28	A4136589	Hs143385	EST1	
36689	28	A4538388	Hs57720	Human mRNA for KIAA0133 gene complete cds	
20982	28	H75655	Hs28884	EST1	
8156	28	D31446	Hs10488	Human sapiens breast/ovary cancer protein 1 (BRCA1) mRNA complete cds	
11362	28	A4272781	Hs20922	EST1	
8613	28	A4459535	Hs31821	EST1	
13986	28	A4478319	Hs5327	EST1	
10303	28	R88178	Hs51187	Alu-like transposon related (includes complementation groups A, C and D)	
21299	28	R33601	Hs28079	EST1	
18217	28	A4030391	Hs28079	EST1	
26355	28	H53168	Hs16488	EST1	
26355	28	H53168	Hs16488	EST1	
21330	28	A4435298	Hs124137	PUTATIVE 80S RIBOSOMAL PROTEIN	
14746	28	L11434	Hs36103	Human chromosome 3p21.1 gene sequence complete cds	
2953	28	D20234	Hs80315	Human mRNA for KIAA0207 gene partial cds	
2953	28	M61828	Hs15200	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR-52) alpha isoform	

**FIGURE 3 (CONT.)**

[illegible]

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## FIGURE 3 (CONT.)

34954	AA31259	EST - RC_A43289	
42556	W74351	Hs 110041 ESTs	
27444	AA32060	Hs 42785 ESTs Weakly similar to F25493.7 [C. elegans]	
21264	R10301	Hs 20564 EST	
8970	AC006265	Hs 8322 Homo sapiens cancer associated surface antigen (RCAS1) mRNA complete cds	
30037	Hs 51652	ESTs	
7602	AA42702	Hs 29835 ESTs Weakly similar to W021812.7 [C. elegans]	
3190	U59184	Hs 78360 HCV nucleoprotein-like tyrosine kinase	
31713	AA41319	Hs 34946 ESTs	
40417	Hs 61006	Hs 85316 Homo sapiens BAC clone RCX002.22 from t(21-q31.1)	
29362	Hs 71781	Hs 103178 ESTs	
35531	AA40963	Hs 111916 ESTs	
20374	N34508	Hs 74014 Phospholipase C beta 4	
18620	F02508	Hs 9417 ESTs	
21097	R00186	Hs 18866 EST	
9940	N71503	Hs 43087 ESTs	
31965	N83629	Hs 93391 ESTs	
15170	U73524	Hs 87485 Human putative ATP/GTP-binding protein (NEAB) mRNA complete cds	
28813	D92257	Hs 61181 Human C-1 mRNA complete cds	
38082	AA482264	Hs 110463 ESTs	
34723	AA287115	Hs 09697 ESTs	
1780	AA282777	Hs 8932 Homo sapiens brain expressed mg finger protein mRNA complete cds	
18973	AA185430	Hs 75643 EST	
30935	U59186	EST - RC_A43269	
18937	F11087	Hs 12544 EST	
3457	S74726	Hs 74204 Angiogenin	
38605	AA58544	Hs 174502 ESTs	
20997	N76086	Hs 35464 ESTs	
24752	Z40012	Hs 21862 Homo sapiens mRNA for KIAA0567 protein complete cds	
28443	AA821611	Hs 70877 ESTs	
432	O38076	Hs 24763 RAN binding protein 1	
11701	AA333031	Hs 31730 Homo sapiens RRM RNA binding protein Gyr-rip (GRR-RBP) mRNA complete cds	
13053	AA458919	Hs 30212 ESTs Weakly similar to 263 proteasome subunit p45 [H. sapiens]	
24822	Z40996	Hs 115441 ESTs	
17872	AA417067	Hs 10055 ESTs	
4890	U53717	Hs 93971 Human osteocalcin stimulating factor mRNA complete cds	
42900	U51779	EST - RC_163179	
34572	AA45499	EST - RC_163179	
35812	AA45499	EST - RC_163179	
6274	X77148	Hs 3796 Glutamate receptor subunit gamma 3	
26395	AA810064	Hs 73602 ESTs	
30390	AA432291	Hs 108527 ESTs Weakly similar to No definition line found [C. elegans]	
21045	N93403	Hs 109441 ESTs	
4559	U14379	Hs 54506 Human dicyclopentyl kinase epsilon DCK mRNA complete cds	
12918	AA427745	Hs 37747 ESTs	
28850	N87514	Hs 28877 ESTs Weakly similar to enfonchocase [H. sapiens]	
28759	Hs 42371	ESTs	
30786	AA435815	Hs 77965 Human Cb-associated RS cyclodextrin CARS-Cyp mRNA complete cds	
21842	N93185	Hs 54911 ESTs	
7097	AA011432	Hs 21840 ESTs	
34662	U50003	Hs 9012 ESTs Weakly similar to AAC-RICH mRNA CLONE AACS PROTEIN (Dipodomys deserti)	
34638	AA432337	Hs 19374 EST - RC_A43257	
37031	AA432638	Hs 40941 ESTs	
6367	Hs 105465	Hs 105465 H repeat mRNA for Sm protein F	
11242	AA222674	Hs 14843 Homo sapiens mRNA for KIAA0704 protein partial cds	
1497	J04086	Hs 3376 Topoisomerase (DNA) II alpha (TOP2A)	
9841	U99724	Hs 95723 Centromere associated C	
11454	AA333554	Hs 23346 ESTs	

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## FIGURE 3 (CONT.)

26920	24	Q04902	Hs 832145	Homo sapiens mRNA for E1B-55kDa-associated protein
26921	24	A04903	Hs 832145	ESTs: Weakly similar to cellular to 5.5 kDa cytosolic protein L311 [H. sapiens]
26922	24	A04904	Hs 832145	Homo sapiens animal tracheal mucus (Hs) complete cds
26923	24	A04905	Hs 832145	ESTs
26924	24	A04906	Hs 832145	ESTs
26925	24	A04907	Hs 832145	ESTs
26926	24	A04908	Hs 832145	ESTs
26927	24	A04909	Hs 832145	ESTs
26928	24	A04910	Hs 832145	ESTs
26929	24	A04911	Hs 832145	ESTs
26930	24	A04912	Hs 832145	ESTs
26931	24	A04913	Hs 832145	ESTs
26932	24	A04914	Hs 832145	ESTs
26933	24	A04915	Hs 832145	ESTs
26934	24	A04916	Hs 832145	ESTs
26935	24	A04917	Hs 832145	ESTs
26936	24	A04918	Hs 832145	ESTs
26937	24	A04919	Hs 832145	ESTs
26938	24	A04920	Hs 832145	ESTs
26939	24	A04921	Hs 832145	ESTs
26940	24	A04922	Hs 832145	ESTs
26941	24	A04923	Hs 832145	ESTs
26942	24	A04924	Hs 832145	ESTs
26943	24	A04925	Hs 832145	ESTs
26944	24	A04926	Hs 832145	ESTs
26945	24	A04927	Hs 832145	ESTs
26946	24	A04928	Hs 832145	ESTs
26947	24	A04929	Hs 832145	ESTs
26948	24	A04930	Hs 832145	ESTs
26949	24	A04931	Hs 832145	ESTs
26950	24	A04932	Hs 832145	ESTs
26951	24	A04933	Hs 832145	ESTs
26952	24	A04934	Hs 832145	ESTs
26953	24	A04935	Hs 832145	ESTs
26954	24	A04936	Hs 832145	ESTs
26955	24	A04937	Hs 832145	ESTs
26956	24	A04938	Hs 832145	ESTs
26957	24	A04939	Hs 832145	ESTs
26958	24	A04940	Hs 832145	ESTs
26959	24	A04941	Hs 832145	ESTs
26960	24	A04942	Hs 832145	ESTs
26961	24	A04943	Hs 832145	ESTs
26962	24	A04944	Hs 832145	ESTs
26963	24	A04945	Hs 832145	ESTs
26964	24	A04946	Hs 832145	ESTs
26965	24	A04947	Hs 832145	ESTs
26966	24	A04948	Hs 832145	ESTs
26967	24	A04949	Hs 832145	ESTs
26968	24	A04950	Hs 832145	ESTs
26969	24	A04951	Hs 832145	ESTs
26970	24	A04952	Hs 832145	ESTs
26971	24	A04953	Hs 832145	ESTs
26972	24	A04954	Hs 832145	ESTs
26973	24	A04955	Hs 832145	ESTs
26974	24	A04956	Hs 832145	ESTs
26975	24	A04957	Hs 832145	ESTs
26976	24	A04958	Hs 832145	ESTs
26977	24	A04959	Hs 832145	ESTs
26978	24	A04960	Hs 832145	ESTs
26979	24	A04961	Hs 832145	ESTs
26980	24	A04962	Hs 832145	ESTs
26981	24	A04963	Hs 832145	ESTs
26982	24	A04964	Hs 832145	ESTs
26983	24	A04965	Hs 832145	ESTs
26984	24	A04966	Hs 832145	ESTs
26985	24	A04967	Hs 832145	ESTs
26986	24	A04968	Hs 832145	ESTs
26987	24	A04969	Hs 832145	ESTs
26988	24	A04970	Hs 832145	ESTs
26989	24	A04971	Hs 832145	ESTs
26990	24	A04972	Hs 832145	ESTs
26991	24	A04973	Hs 832145	ESTs
26992	24	A04974	Hs 832145	ESTs
26993	24	A04975	Hs 832145	ESTs
26994	24	A04976	Hs 832145	ESTs
26995	24	A04977	Hs 832145	ESTs
26996	24	A04978	Hs 832145	ESTs
26997	24	A04979	Hs 832145	ESTs
26998	24	A04980	Hs 832145	ESTs
26999	24	A04981	Hs 832145	ESTs
27000	24	A04982	Hs 832145	ESTs

## FIGURE 3 (CONT.)

15352	23	AA154943	Hs 20911	ESTs	
15664	23	W61756	Hs 56308	ESTs	Moderately similar to YY1-associated factor-2 [H sapiens]
26583	23	AA278774	Hs 142497	ESTs	
37134	23	AA154149	Hs 99357	ESTs	
7833	23	AA249300	Hs 7048	ESTs	
3874	23	U95237	Hs 89872	Human testis AU-50-related clone 1 (f AC1) mRNA complete cds	
3894	23	Z86770	Hs 71623	ESTs	
11178	23	AA197596	Hs 20848	ESTs	
18877	23	AA064816	Hs 56883	ESTs	
18799	23	H57330	Hs 37430	EST	
5946	23	X63337	EST - X63337		
72077	23	U95316	Hs 78770	Human testis RNA, poly(A) <sup>+</sup>	
32077	23	Hs 78770	Human testis RNA, poly(A) <sup>+</sup>		
32077	23	Hs 78770	Human testis RNA, poly(A) <sup>+</sup>		
40970	23	Hs 78770	Human testis RNA, poly(A) <sup>+</sup>		
6975	23	X58105	Hs 83383	ESTs	Moderately similar to the AU SUBFAMILY SX WARNING ENTRY (H sapiens)
22255	23	R00777	Hs 83383	ESTs	Membrane cofactor protein (CD46) epidermal-type cytoplasmic cDNA sequence (antigen)
9671	23	J05032	Hs 60768	ASPARTYL-TRNA SYNTHETASE	
9739	23	D78100	Hs 83108	ESTs	
41997	23	T47788	Hs 109628	ESTs	
31105	23	H93207	Hs 46735	EST	
38545	23	F04320	Hs 33120	Replication factor C, 37 kD subunit	
7404	23	AA091889	Hs 7381	Human spleen vesicle dependent ion channel protein mRNA complete cds	
6358	23	X55373	Hs 77496	H sapiens mRNA for 6m protein G	
26763	23	K01952	Hs 103747	ESTs	Moderately similar to HYPOTHETICAL 66.3 KD PROTEIN P02A9.3 IN CHROMOSOME 18 (Caenorhabditis elegans)
14528	23	AA020207	Hs 27378	ESTs	
11197	23	R07320	Hs 19928	ESTs	
32107	23	Hs 19928	Hs 19928	ESTs	
38320	23	AA490611	Hs 99838	ESTs	
41875	23	R88333	Hs 10480	ESTs	
4674	23	U54199	Hs 83121	Human (GH) protein mRNA complete cds	
26661	23	D60037	Hs 45129	EST	Weakly similar to C50B8.3 (C. elegans)
31002	23	N62827	Hs 48845	ESTs	
28750	23	AA233832	Hs 88619	ESTs	
11567	23	AA236717	Hs 30327	Human islet amyloid polypeptide (IAPP) mRNA complete cds	
25050	23	AA011134	Hs 25893	ESTs	Weakly similar to mme (H sapiens)
41935	23	T76681	Hs 75781	Human serum albumin mRNA complete cds	
29815	23	AA327853	Hs 42850	H sapiens mRNA for 4.6 kDa phosphoglucomutase	
40545	23	K04881	Hs 104929	Human spleen mRNA for K04A059 protein perlecan	
3343	23	W55994	Hs 109903	ESTs	
42435	23	Hs 109903	Hs 109903	ESTs	
31241	23	R06817	Hs 20180	ESTs	
25796	23	AA133668	Hs 95788	ESTs	Reproductive group (neofunctional chromosome) protein 2
34184	23	AA237859	Hs 32380	Human cyclinase protease 4/20 isoform alpha (p40/2) mRNA complete cds	
8672	23	AA477045	Hs 59338	ESTs	
7387	23	AA093917	Hs 71475	ESTs	
28822	23	D53352	Hs 62624	ESTs	
18018	23	AA173223	Hs 44426	ESTs	
20843	23	N63532	Hs 56853	Human spleen mRNA for ATP-dependent RNA helicase 848 complete cds	
10054	23	R10208	Hs 120997	ESTs	Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PHA0-PAC2 INTERGENIC REGION (Schistosoma cercariae)
34094	23	AA000008	Hs 104139	ESTs	
41248	23	R17796	Hs 23240	ESTs	
27834	23	R28537	Hs 103329	ESTs	
19086	23	H46502	Hs 28212	ESTs	
25586	23	AA286509	Hs 111695	ESTs	Weakly similar to K02822.3 gene product (C. elegans)
20909	23	AA000002	Hs 104139	ESTs	Human 25S protein same as estimated part (human) (P0H1) mRNA complete cds
851	23	N71104	Hs 4310	EST - D78129	
40409	23	H98837	Hs 82951	Human spleen support mRNA complete cds	
20340	23	N38813	Hs 30559	ESTs	



## FIGURE 3 (CONT.)

5273	21	U53343	EST - U53343	
37415	21	AA53207	Hs 99348 EST	
14592	21	AA521340	Hs 100502 EST: Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MID-UPSTREAM INTERGENIC REGION [Saccharomyces cerevisiae]	
17376	21	AA531447	Hs 93417 ESTs	
17387	21	AA531745	Hs 122881 ESTs: Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]	
5179	21	U81554	Hs 5171 Homo sapiens signal recognition particle 72 (SRP72) mRNA complete cds	
40028	21	H63231	Hs 100332 Homo E2 ubiquitin-conjugating enzyme Ubch10B (UBCH10B) mRNA complete cds	
19972	21	H53039	Hs 33376 ESTs	
22301	21	H53847	Hs 13034 ESTs	
20545	21	H53866	Hs 140318 ESTs	
20546	21	H53866	Hs 140318 ESTs	
3441	21	H53866	Hs 140318 ESTs	
41893	21	H53866	Hs 140318 ESTs	
39798	21	H53866	Hs 140318 ESTs	
30021	21	H53866	Hs 140318 ESTs	
8382	21	AA424199	Hs 1005239 ESTs: Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521 [H. sapiens]	
28288	21	AA538447	Hs 83951 ESTs: Weakly similar to C50B5.3 [C. elegans]	
5507	21	H532740	Hs 78656 5' nucleotidase (CD73)	
19747	21	H53372	Hs 32407 ESTs	
28155	21	AA480777	Hs 055698 ESTs	
924	21	G1102-RT11112	EST - HG1112-RT11112	
5544	21	H72639	Hs 35182 ESTs	
8384	21	AA424282	Hs 81728 Human 75-kD autoantigen (PM-55k1) mRNA complete cds	
21183	21	AA427837	Hs 20705 Reticuloplasmin 3 [C. elegans neostoma]	
21246	21	H53869	Hs 17189 Ropomycin ribonuclease (Ropomycin)	
35340	21	AA388900	Hs 35075 ESTs: Weakly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]	
10886	21	AA132063	Hs 15313 ESTs: Weakly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]	
381	21	D18473	Hs 78170 Intracellular RNA synthase	
22051	21	R49047	Hs 31975 ESTs: Weakly similar to [H. ALU SUBFAMILY J] WARNING ENTRY m [H. sapiens]	
3293	21	M84593	Hs 2051 Taste specific protein Y-50kD	
11528	21	AA336018	Hs 10724 ESTs: Weakly similar to unknown [S. cerevisiae]	
11890	21	AA378333	Hs 17481 Homo sapiens clone 24502 mRNA sequence	
13843	21	AA455378	Hs 15017 Homo sapiens clone 24477 mRNA sequence	
19927	21	H71829	Hs 33701 ESTs	
36511	21	AA429032	Hs 121018 ESTs	
2130	21	L04007	Hs 81731 Homo sapiens thyroid receptor interactor (TRIP9) gene complete cds	
1193	21	AA080768	Hs 48476 Homo sapiens clone 1046 C14-ORF1 region mRNA	
414	21	AA131333	Hs 09037 ESTs	
32946	21	AA131333	Hs 09037 ESTs	
7525	21	AA149359	Hs 89041 ESTs	
36502	21	F09351	Hs 16492 ESTs: Weakly similar to S. cerevisiae P141 nuclease [C. elegans]	
28028	21	AA426419	Hs 11992 ESTs	
18425	21	AA332103	Hs 59112 ESTs	
25494	21	T70045	Hs 18887 ESTs: Weakly similar to HYPOTHETICAL 33.2 KD PROTEIN F28A3.7 IN CHROMOSOME 1 [C. elegans]	
30882	21	H56906	Hs 47896 EST	
22597	21	T47333	Hs 77798 Human TFIID subunit TAF155 (TAF155) mRNA complete cds	
31360	21	W60314	Hs 47283 ESTs	
10259	21	R77327	Hs 29845 ESTs	
21832	21	R43365	Hs 22773 ESTs	
20580	21	N58148	Hs 34227 ESTs	
12907	21	AA427377	Hs 26502 ESTs	
22146	21	T10284	Hs 119722 ESTs	
41904	21	U01814	Hs 3353 Homo sapiens nuclear receptor homolog RPOJ mRNA complete cds	
41910	21	AA538433	Hs 17101 ESTs: Homo sapiens mRNA for Cdc7-related kinase complete cds	
38	21	AA538433	Hs 17101 ESTs	
14340	21	H21880	Hs 43047 ESTs	
29840	21	AA113149	Hs 81330 Homo sapiens SPL (PL) mRNA complete cds	
23570	21	AA113149	Hs 81330 Homo sapiens SPL (PL) mRNA complete cds	
28071	21	AA336850	Hs 118370 Protein phosphatase 2A regulatory subunit B, alpha-1	

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FIGURE 3 (CONT.)

21	AA215584	Hs 88461	EST	
21	AA381293	Hs 23719	ESTs	
21	F10077	Hs 12695	ESTs	
21	F89385	Hs 90182	H sapiens mRNA for SAT3B protein	
21	U08971	Hs 2810	Phosphoserine phosphatase synthase 2	
21	R48483	Hs 5637	ESTs	
21	AA256842	Hs 24908	ESTs	
21	R12680	Hs 140902	ESTs	
21	Z14387	Hs 1370	Histamine receptor H1	
21	AA065358	Hs 63314	ESTs	
21	AA481603	Hs 10713	ESTs	
21	U08372	Hs 63560	Human telomerase protein (TP) Hs-gamma mRNA complete cds	
21	W07448	Hs 41241	ESTs	
21	R10576	Hs 21590	ESTs	Moderately similar to Hs ALU SUBFAMILY SX WARNING ENTRY (H sapiens)
21	AA234935	Hs 65032	ESTs	
21	Z32911	Hs 12299	Homo sapiens GTP-1, Accessory phosphatase (GTPase) mRNA complete cds	
21	AA481148	Hs 105157	ESTs	
20	AC022113	Hs 63379	Cyclochrome c oxidase subunit VIIb	
20	281625	Hs 77324	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1	
20	AA323147	EST - AA323147	EST - AA323147	
20	AA231400	Hs 3850	ESTs	Highly similar to RAS-RELATED PROTEIN RAB-10 (C. elegans)
20	AA442101	Hs 5049	Tyrosine 3-oxoindolepyruvate decarboxylase (TPO) protein beta polypeptide	
20	AA480551	Hs 12171	H sapiens mRNA for nuclear protein SA-2	
20	W88372	Hs 50548	ESTs	
20	AA460575	Hs 31748	Human DNA sequence from defined TGS11 on chromosomes 8, Contains Dase BING1 T repeat RGLJ K22 BING4 BING3 ESTs and CDS inserts	
20	AA460575	Hs 42785	H sapiens mRNA for putative RNA helicase 3 and	
20	U08951	Hs 112180	Zinc finger protein 143 (p42.52)	
20	D18811	Hs 88268	Coproporphyrinogen decarboxylase (COPD) protein (S. cerevisiae)	
20	AA418921	Hs 10325	ESTs	Highly similar to RSP3 PROTEIN [Saccharomyces cerevisiae]
20	D30966	Hs 28591	ESTs	Highly similar to TRANSLOCIN-ASSOCIATED PROTEIN GAMMA SUBUNIT [Rattus norvegicus]
20	AA147425	EST - AA147425_3	EST - AA147425_3	
20	D58234	Hs 12452	ESTs	
20	Q26413	Hs 45837	EST - D26413	
20	Hs 9539	Hs 45837	ESTs	
20	D47228	Hs 73718	Holoenzyme synthetase (beta-primase)-Catecholase A-subunit (ATP-hydrolyzing) (S. cerevisiae)	
20	U10825	Hs 13285	ESTs	Highly similar to HYPOTHETICAL PROTEIN H0004 [Haemophilus influenzae]
20	U10825	Hs 2131	Arginine vasopressin receptor 1 (AVPR1)	
20	RN1384	Hs 2131	EST - RC_891384	
20	D33864	Hs 12452	EST - D33864	
20	C31183	Hs 66609	EST	
20	AA256878	Hs 17035	ESTs	Highly similar to POP3 PROTEIN [Saccharomyces cerevisiae]
20	AA475233	Hs 11813	ESTs	Highly similar to Hs ALU SUBFAMILY J WARNING ENTRY (H sapiens)
20	Z33349	Hs 18575	ESTs	Highly similar to VACUOLAR ATP SYNTHASE SA NO SUBUNIT [Saccharomyces cerevisiae]
20	AA122217	Hs 18643	ESTs	Highly similar to HYPOTHETICAL 913 NO PROTEIN F2885 IN CHROMOSOME III [C. elegans]
20	AA479648	Hs 147820	ESTs	
20	W07531	Hs 12342	Homo sapiens clone 74528 mRNA sequence	
20	AA409710	Hs 42582	ESTs	
20	AA442598	Hs 21198	ESTs	Highly similar to MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR [Neurospora crassa]
20	AA409922	Hs 135552	ESTs	Highly similar to The KIAA1181 gene product (H sapiens)
20	H10841	Hs 5960	EST - RC_470041	
20	H10841	Hs 5960	ESTs	
20	W07276	Hs 77276	Human clone 121711 indicates nuclear transposon (Hmud2) mRNA sequence	
20	H83535	Hs 3633	Homo sapiens clone 121711 indicates nuclear transposon (Hmud2) mRNA sequence	
20	D53778	Hs 77098	Human mRNA for Hmud2 (Hmud2) gene product	
20	AA163528	Hs 3633	Human clone 121711 indicates nuclear transposon (Hmud2) mRNA sequence	
20	AA171728	Hs 101590	ESTs	
20	A58244	Hs 74107	Zinc finger protein 43 (MTF8)	
20	AA435107	Hs 91018	ESTs	
20	AA126951	Hs 10957	ESTs	Highly similar to DNA directed RNA polymerase (D. melanogaster)
20	AA018907	Hs 5427	ESTs	

FIGURE 3 (CONT.)

8118	20	AA325921	M1.16458	ESTs
27982	20	NC5228	M1.21543	ESTs
32236	20	R18127	M1.57435	Natural resistance-associated macrophage protein 2
3279	20	U84063	M1.64925	DIHYDROOROTATE DEHYDROGENASE PRECURSOR
18235	20	AA813249	M1.60627	ESTs
32972	20	AA178215	EST - RC_AA178215	
41256	20	R31377	M1.30598	ESTs
34324	20	AA292655	M1.96557	ESTs
23169	20	133215	M1.117223	ESTs
29851	20	M21145	M1.43094	ESTs
32662	20	W25218	M1.55510	EST

## FIGURE 4

Accession	UniGene	UniGene Description
U03778	U03778	Protease inhibitor 5 (maize)
U03779	U03779	Human sapiens clone Z197 and Z2917 mRNA partial cds
U03780	U03780	ESTs
U03781	U03781	Human protein-tyrosine phosphatase (HPTP-1) mRNA partial sequence
U03782	U03782	Ribonuclease L (7'S oligonucleotide synthetase-dependent) inhibitor
U03783	U03783	ESTs
U03784	U03784	Human mRNA for transcriptional activator HNF7b complete cds
U03785	U03785	ESTs
U03786	U03786	ESTs
U03787	U03787	ESTs
U03788	U03788	ESTs
U03789	U03789	ESTs
U03790	U03790	ESTs
U03791	U03791	ESTs
U03792	U03792	ESTs
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U03801	U03801	ESTs
U03802	U03802	ESTs
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U04119	U04119	ESTs
U04120	U04120	ESTs
U04121	U04121	ESTs
U04122	U04122	ESTs
U04123	U04123	ESTs
U04124	U04124	ESTs

## FIGURE 4 (CONT.)

26355	AA256378	Hs.09781	ESTs	Hs.14732	MALATE OXIDOREDUCTASE
4455	U43844	Hs.14543	ESTs	Hs.14543	ESTs
10748	AA055892	Hs.4770	ESTs	Hs.4770	ESTs
8111	AA323787	Hs.31754	EST	Hs.22355	ESTs
19389	H20165	R34771	EST	Hs.12013	Ribonuclease L (2'S-dephosphadenylate synthetase-diphosphate) inhibitor
32185	R27875	R27875	EST	Hs.118976	ESTs
21519	X74887	R01654	ESTs	Hs.118977	Proteoglycan convertase subunit/lysozyme type 1
41107	R01654	X54810	ESTs	Hs.78877	ESTs
6187	X54810	AA23052	ESTs	Hs.16399	ESTs
5986	AA23052	U57341	EST	Hs.16399	ESTs
11653	U57341	F04022	ESTs	Hs.27883	ESTs
4702	F04022	V07277	ESTs	Hs.17546	ESTs
19876	V07277	U57771	ESTs	Hs.17546	ESTs
24197	U57771	AA504462	ESTs	Hs.81771	Human L-lysine aminohydrolase mRNA complete cds
4713	AA504462	AA216722	ESTs	Hs.105730	ESTs
38460	AA216722	F69739	ESTs	Hs.54481	Human mRNA for apolipoprotein E receptor 2 complete cds
18330	Z92394	Z92394	ESTs	Hs.12562	ESTs
18782	F69739	AA181348	ESTs	Hs.94432	ESTs
42766	AA181348	AA054438	ESTs	Hs.94432	ESTs
34014	AA054438	H23003	ESTs	Hs.96178	ESTs
16835	H23003	AA184789	ESTs	Hs.60753	ESTs
29693	AA184789	HQ3344-H73521	EST	Hs.42146	ESTs
11180	HQ3344-H73521	AA259158	ESTs	Hs.26006	ESTs
1158	AA259158	AA125223	ESTs	EST - HQ3344-H73521	
11813	AA125223	X54925	ESTs	Hs.22153	ESTs
10992	X54925	AA065300	ESTs	Hs.22900	ESTs
16993	AA065300	AA132750	ESTs	Hs.22900	ESTs
17654	AA132750	D52892	ESTs	Hs.62180	ESTs
39436	D52892	H52702	ESTs	Hs.62180	ESTs
19727	H52702	R42278	ESTs	Hs.74574	ESTs
41381	R42278	R79111	ESTs	Hs.36590	ESTs
22576	R79111	AA408206	ESTs	Hs.31748	ESTs
35768	AA408206	AA180223	ESTs	Hs.29388	ESTs
33980	AA180223	AA446486	ESTs	Hs.104746	ESTs
37084	AA446486	AA347193	ESTs	Hs.8454	ESTs
26935	AA347193	L42778	EST	Hs.125129	ESTs
2168	L42778	U39817	ESTs	Hs.77831	ESTs
4302	U39817	D30037	ESTs	EST - L42778	
9127	D30037	X17644	ESTs	Hs.36820	ESTs
20614	X17644	U0714	ESTs	Hs.91447	ESTs
5632	U0714	U01157	ESTs	Hs.18937	ESTs
4388	U01157	Z38462	ESTs	Hs.2707	ESTs
3598	Z38462	AA454632	ESTs	Hs.109831	ESTs
24545	AA454632	AA004104	ESTs	Hs.165	ESTs
37456	AA004104	AA031268	ESTs	Hs.12403	ESTs
10840	AA031268	AB000905	ESTs	Hs.123157	ESTs
25179	AB000905	F09458	ESTs	Hs.30177	ESTs
21	F09458	W65423	ESTs	Hs.113319	ESTs
39232	W65423	R52831	ESTs	Hs.143080	ESTs
42902	R52831	AA027069	ESTs	Hs.12421	ESTs
23272	AA027069	H52949	ESTs	Hs.112898	ESTs
39110	H52949	H542115	ESTs	Hs.105413	ESTs
16410	H542115			Hs.28306	ESTs
29845				Hs.20563	ESTs
				Hs.125849	ESTs
				Hs.42115	ESTs

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## FIGURE 4 (CONT.)

36405	AA020405	Hs 10601	Homo sapiens mRNA for KIAA0530 protein partial cds
4029	U21090	Hs 74598	Human DNA polymerase delta small subunit mRNA complete cds
15065	U30246	Hs 110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
40524	N35386	Hs 112297	ESTs
31484	N68466	Hs 49683	ESTs
38801	AA598720	Hs 109041	ESTs
40531	N45124	Hs 6809	ESTs
236	D13645	Hs 2471	Human mRNA for KIAA0020 gene complete cds
35803	AA410205	Hs 87911	ESTs
18591	H06649	Hs 33785	ESTs
36828	AA608177	Hs 109363	ESTs
35798	AA410231	Hs 98069	ESTs
3163	M84424	Hs 1355	Cathepsin E
22400	R94109	Hs 22487	ESTs
39082	AA620333	Hs 112857	ESTs
25082	AA017257	Hs 101139	ESTs
5637	X58377	Hs 1721	Human mRNA for adipoonectin inhibitory factor
5214	U83303	Hs 120029	H. sapiens mRNA for granulocyte chemotactic protein
36958	NA9104	Hs 87507	ESTs
40960	AA42080	Hs 79108	NUCLEAR FACTOR RFP140
25951	AA334556	Hs 135156	EST
22072	R04006	Hs 28410	ESTs
39832	H58279	EST - RC_H00279	EST - RC_H00279
23198	T40530	Hs 8241	ESTs Weakly similar to B0033.14 [C. elegans]
29331	H68116	Hs 33063	ESTs
38316	AA493500	Hs 18747	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds
37829	AA470884	Hs 98356	ESTs
3670	U14518	Hs 1594	Centromere protein A (17kD)
38176	AA621091	Hs 72087	ESTs
41793	T03687	Hs 7207	ESTs
32277	R61483	Hs 26686	Human mRNA for rod photoreceptor protein complete cds
5358	X07876	Hs 89781	Wingless-type MMTV integration site 2 human homolog
6382	X85133	Hs 85273	H. sapiens RBO-1 mRNA
41040	N91948	Hs 175004	ESTs
35000	AA820532	EST - RC_AA820532	EST - RC_AA820532
20307	N34830	Hs 37636	ESTs
18760	AA309801	Hs 86277	ESTs
41063	N93618	Hs 28554	ESTs
33109	V05961	Hs 22564	Human mRNA for KIAA0369 gene complete cds
28015	AA477421	Hs 21861	ESTs
30610	N50138	Hs 47002	EST
34015	AA101353	Hs 109884	ESTs
40559	N33024	Hs 22450	ESTs
1445	J00027	Hs 72885	MHC class I protein HLA-G
13242	AA445994	Hs 21331	ESTs
17080	AA479248	Hs 52871	H. sapiens mRNA for SY1
42342	T89278	Hs 79353	Homo sapiens E2F-related transcription factor (DP-1) mRNA complete cds
37135	AA447540	Hs 99112	EST
20964	N55443	Hs 23625	ESTs
28141	AA468432	Hs 58407	ESTs
21240	R06613	Hs 20188	ESTs
34382	AA325512	Hs 10069	ESTs
25946	AA324365	Hs 102456	Homo sapiens survival of motor neuron protein interacting protein 1 (SIP1) mRNA complete cds
40813	N69218	Hs 108232	ESTs
35597	AA405312	Hs 104741	ESTs
34672	AA384372	Hs 111471	ESTs

## FIGURE 4 (CONT.)

3659	U04313	Hs 55278	Protease inhibitor 5 (mesalin)
17051	AA070801	Hs 51615	ESTs
19203	H11593	Hs 26116	ESTs
20791	N86057	Hs 80357	Human sapiens telomeric repeat binding factor (TRF-1) mRNA complete cds
24215	W69425	Hs 15787	ESTs
37246	AA449311	Hs 98650	Human sapiens ribotic checkpoint protein kinase (RUB1) mRNA complete cds
6700	Y12394	Hs 3886	Human sapiens importin-alpha homolog (SRP1/gamma) mRNA complete cds
25906	AA149007	Hs 103871	EST
36307	AA424803	Hs 98474	EST
25047	AA011031	Hs 110182	ESTs
33343	W76834	Hs 55559	ESTs Weakly similar to nucleolin [H. mutans]
5799	X55330	Hs 111661	Aspartylglucosaminidase
22973	T64047	Hs 15428	ESTs
29573	H88353	Hs 135212	ESTs Weakly similar to hsa-1 protein ORF2 [H. sapiens]
26391	AA410291	Hs 142179	ESTs
40084	H12283	Hs 114121	ESTs
29795	N70641	Hs 38483	Human mRNA for KIAA0285 gene partial cds
5560	X53575	Hs 46230	ESTs Highly similar to HYPOTHETICAL MYELOID CELL LINE PROTEIN 3 [Homo sapiens]
37811	AA456996	Hs 85512	ATPase Ca++ transporting plasma membrane 2 (NOTE: resubmission of symbol)
25274	AA435011	Hs 53970	Human signaling lymphocytic activation molecule (SLAM) mRNA complete cds
37168	AA417772	Hs 88758	ESTs
38433	D27037	Hs 15153	ESTs
1570	K01383	Hs 35650	Human tyrosine kinase 2 (TYK2) mRNA complete cds
30617	N50648	Hs 47083	ESTs
35106	AA371561	Hs 142553	EST Weakly similar to putative p150 [H. sapiens]
789	D86971	Hs 78651	Human mRNA for KIAA0217 gene partial cds
4386	U06022	Hs 21523	DNA repair protein XRCC4
31944	N93193	Hs 80310	ESTs
13227	L72611	Hs 142492	ESTs Weakly similar to [H. ALU SUBFAMILY J WARNING ENTRY III] [H. sapiens]
4157	L03996	Hs 78979	Human cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA complete cds
2123	AA342402	Hs 28956	Human sapiens (clone 427171) mRNA fragment
26926	X91653	Hs 48729	EST - X91653
6479	AA260670	Hs 24968	ESTs
11869	AA458664	Hs 102848	ESTs
37601	D12163	Hs 103262	ESTs
29844	N38893	Hs 28578	Human sapiens KIAA0426 mRNA complete cds
40004	U16281	Hs 86578	Human MDA-7 (mda-7) mRNA complete cds
3913	T90313	Hs 18732	ESTs
23759	AA56597	Hs 2173	fluorocytidine kinase 4 (repha (13) fluorocytidine kinase myeloid-specific)
2857	AA278721	Hs 103104	ESTs
34518	AA171895	Hs 30057	Human sapiens clone 24749 and 24750 mRNA sequences
18008	H02980	Hs 28685	ESTs
19001	D60831	Hs 126021	ESTs
39488	T55531	Hs 141905	ESTs
23390	AA207123	Hs 130857	ESTs
39171	AA485724	EST - RC_AA485724	
20080	F13655	Hs 65638	ESTs Moderately similar to [H. ALU SUBFAMILY S81 WARNING ENTRY III] [H. sapiens]
9773	L44542	Hs 126923	ESTs
25215	AA035340	Hs 1255	APOLIPROTEIN A1 REGULATORY PROTEIN-1
39218	AA821330	Hs 114381	ESTs
20089	N70054	Hs 20325	ESTs Weakly similar to putative p150 [H. sapiens]
33713	Z39427	Hs 65748	ESTs
18392	AA237751	Hs 55698	ESTs
42390	V040150	Hs 24483	Human sapiens chromosome-associated polypeptide (HCAp) mRNA complete cds

## FIGURE 4 (CONT.)

35493	AA405485	Hs.106514	EST1 Weakly similar to similar to complex testis-specific protein [C. elegans]
35500	AA400715	Hs.107479	EST1
1856	L18520	Hs.36580	MELANOMA-ASSOCIATED ANTIGEN 2
36758	AA425962	Hs.108465	EST1 Weakly similar to ctn ALU SUBFAMILY J WARNING ENTRY (H. sapiens)
37068	AA443132	Hs.22143	EST1 Weakly similar to ctn ALU CLASS C WARNING ENTRY (H. sapiens)
37070	W66891	Hs.55868	EST1 Weakly similar to polyphosphate N-acetylglucosaminyltransferase (H. sapiens)
27037	AA400198	Hs.93753	EST1
49027	N61051	Hs.48570	Homo sapiens Werner syndrome gene complete cds
3375	S50723	Hs.108643	HNR-11
37310	AA451707	Hs.99248	EST1
36235	AA469030	Hs.105323	EST1
22254	R56432	Hs.26538	EST1
36945	AA436188	Hs.103902	EST1
28323	AA599339	Hs.50718	EST1
30207	N33920	Hs.44532	H. sapiens mRNA for diaphanin
8454	X92889	Hs.55823	H. sapiens mRNA for UDP-GalNAc 4-epimerase N-acetylglucosaminyl transferase
36268	AA421592	Hs.94623	EST1
37546	AA459641	Hs.99433	EST1
4183	U31116	Hs.17750	Human beta-actin/actin A3b mRNA complete cds
37777	AA434860	Hs.11534	Homo sapiens JAK2 kinase mRNA complete cds
36280	AA487891	Hs.79506	EST - RC_AA487891
3243	AA15351	Hs.102714	EST1
39045	AA610077	Hs.111914	EST1
35495	AA405327	Hs.21401	Scaven tyrosine kinase
2322	S86207	Hs.21420	EST1
22282	T925197	Hs.61070	EST1
32740	T92520	Hs.124018	EST1
37657	AA426151	Hs.96297	EST1
41101	AA426188	Hs.58174	EST1
34191	AA335703	Hs.485	Reptagene E receptor 3 (subtype EP3) (alternative products)
33301	V07380	Hs.6592	EST1
7785	C86096	Hs.75530	AFFLHJMTFR6M11507_5
34070	AA198540	Hs.87365	EST1
35990	AA336356	Hs.58940	EST1
32777	AA336985	Hs.26524	EST1
25801	AA148530	Hs.80901	DNA polymerase gamma
34254	R55823	Hs.55209	EST1 Moderately similar to OMP-40 PROTEIN (H. sapiens)
34054	AA480016	Hs.177256	Human enhancer of rease homolog 2 (E2H2) mRNA complete cds
37034	P86926	Hs.9959	Repression factor C (enhancer 1) 3 (3800)
4787	U61145	Hs.22226	EST1
1694	L07541	Hs.171688	EST1
18718	P04915	Hs.95527	EST1
40427	N21147	Hs.171688	EST1
32635	T81116	Hs.177	Homo sapiens placental CD-PDE mRNA complete cds
4308	U38798	Hs.142638	EST1
35211	AA486687	Hs.78653	URACIL DNA GLYCOSYLASE 4 PRECURSOR
6438	X89336	Hs.141444	EST1
36590	AA595545	Hs.28736	Homo sapiens mRNA for TRAF5 complete cds
4945	U69108	Hs.2001	THROMBOXANE SYNTHASE
41854	R76437	Hs.20116	EST1
41163	R08176	Hs.104328	EST1
34400	AA353400	Hs.104768	EST1
35872	AA411144	Hs.104768	EST1

## FIGURE 4 (CONT.)

26926	AA280641	Hs 40128	ESTs highly similar to 60S RIBOSOMAL PROTEIN L39 [Rattus norvegicus]
40704	H88296	EST - RC_H88296	
19164	H10395	Hs 30950	EST
26740	AA272282	Hs 90439	Human mRNA for KIAA0152 gene complete cds
6963	AF043737	AF043737	AF043737 Human mRNA for KIAA0152 gene complete cds
35322	AA398710	Hs 67195	M. sapiens RNA for CLN3
1210	HG37-HT37	EST - HG37-HT37	
22793	R60208	Hs 35333	ESTs
30052	AA117027	Hs 104787	EST
26574	AA279504	Hs 88929	ESTs
35197	AA398120	Hs 97504	ESTs
37976	AA479295	Hs 100290	ESTs highly similar to RING CANAL PROTEIN [Drosophila melanogaster]
4062	U65437	Hs 95638	Human homeodomain-containing protein (HNF) mRNA complete cds
26700	AA282187	Hs 88002	EST
35049	AA350657	Hs 22507	ESTs
40063	H73466	Hs 79088	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3
17541	AA127459	Hs 108768	ESTs
19948	H16263	Hs 124151	ESTs
4477	U45860	Hs 37137	Human LAP-like protein (LAP) mRNA complete cds
26916	AA331383	Hs 47378	ESTs
34186	AA228030	Hs 120234	ESTs
29229	H48458	Hs 36322	Human mRNA for KIAA0180 gene complete cds
42773	YEL0190MMS21	EST - YEL0190MMS21	
32189	R43163	Hs 95044	ESTs
36738	AA435610	EST - RC_AA435610	
25545	H66831	Hs 49268	EST
25925	R43872	Hs 86547	ESTs
29344	AA164494	Hs 22891	EST
1346	H66839	Hs 29417	ESTs highly similar to CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-4 [H. sapiens]
218	HG4716-HT5158	Hs 38782	EST
26100	D13540	EST - HG4716-HT5158	
41593	AA242835	Hs 5517	PROTEIN-TYROSINE PHOSPHATASE 2C
42290	R64129	Hs 143745	ESTs
6713	T55105	Hs 142670	ESTs
33377	Y08564	EST - Y08564	
31618	H61219	Hs 42636	ESTs highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 [C. elegans]
26718	N73449	Hs 50273	ESTs
21556	AA282576	Hs 49407	ESTs
40113	R33112	Hs 100469	human AF 6 mRNA complete cds
10801	AA069283	Hs 15266	ESTs
37491	AA455239	Hs 9922	ESTs highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 [C. elegans]
254	D1457	Hs 81892	ESTs highly similar to CHROMOSOME CONDENSATION PROTEIN CPV-27 [Caenorhabditis elegans]
26693	H97819	Hs 42453	ESTs
13110	AA435643	Hs 43881	ESTs
54663	AA289784	Hs 19114	Human sapiens mRNA for high mobility group protein HMGB2
39432	D51691	Hs 88941	EST
31572	N71294	Hs 82285	Phosphoribosylpyrimidine formyltransferase phosphoribosylpyrimidine synthetase phosphoribosylpyrimidine synthetase
17903	AA160259	Hs 110324	ESTs
20747	H66842	Hs 72354	EST
4676	U55206	Hs 19395	ESTs
34383	AA231567	Hs 78619	Human sapiens glutamine-glutaryl hydrolase (GGH) mRNA complete cds
39094	AA570036	Hs 108071	Human sapiens mRNA for KIAA0530 protein partial cds
3988	U15126	Hs 112264	ESTs
		Hs 36373	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds

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## FIGURE 4 (CONT.)

39386	85	D12184	Hs 3350	ESTs	Hs 3350	ESTs	Human DP prostanoid receptor (PTGDM) mRNA partial cds
4192	84	U31099	Hs 121478	Human putative calcium influx channel (hirc3) mRNA complete cds	Hs 121478	Human putative calcium influx channel (hirc3) mRNA complete cds	
4507	84	U47050	Hs 24852	Human putative calcium influx channel (hirc3) mRNA complete cds	Hs 24852	Human putative calcium influx channel (hirc3) mRNA complete cds	
35698	94	AA02227	Hs 87345	ESTs	Hs 87345	ESTs	Moderately similar to N-tropomodulin [R: noneglect]
18829	93	H56613	Hs 37628	EST	Hs 37628	EST	
14837	93	T40145	Hs 21821	ESTs	Hs 21821	ESTs	
17336	93	AA099585	Hs 41175	ESTs	Hs 41175	ESTs	
29498	92	H85434	Hs 40673	EST	Hs 40673	EST	
29043	92	N24780	Hs 42983	ESTs	Hs 42983	ESTs	Moderately similar to III ALU SUBFAMILY J WARNING ENTRY III [H: sapiens]
17997	91	AA169833	Hs 72835	EST	Hs 72835	EST	
13983	91	AA470917	Hs 34827	ESTs	Hs 34827	ESTs	Weakly similar to No definition line found [C: elegans]
30538	91	N49071	Hs 83568	ESTs	Hs 83568	ESTs	
26380	91	AA257012	Hs 88054	EST	Hs 88054	EST	
40812	90	N53419	Hs 83389	ESTs	Hs 83389	ESTs	
903	90	D90070	Hs 96	ATL-derived PMA-responsive (APR) peptide	Hs 96	ATL-derived PMA-responsive (APR) peptide	
22874	90	887150	Hs 13865	ESTs	Hs 13865	ESTs	
12746	89	N02904	Hs 8007	ESTs	Hs 8007	ESTs	
19466	89	AA029847	Hs 82489	ESTs	Hs 82489	ESTs	
19632	88	H47391	Hs 33947	ESTs	Hs 33947	ESTs	
3544	88	M35697	Hs 81594	Primer dimer 4	Hs 81594	Primer dimer 4	
2726	88	AA237121	Hs 105933	Human prolyl-4-hydroxylase mRNA complete cds	Hs 105933	Human prolyl-4-hydroxylase mRNA complete cds	
39939	88	H53454	Hs 110291	ESTs	Hs 110291	ESTs	EST - RC_H53454
25111	87	AA078787	Hs 25278	ESTs	Hs 25278	ESTs	
21655	87	P38239	Hs 26733	ESTs	Hs 26733	ESTs	Weakly similar to C36B1.3 [C: elegans]
27074	86	AA401475	Hs 87825	Human transferrin (TFN) mRNA complete cds	Hs 87825	Human transferrin (TFN) mRNA complete cds	
4659	85	U03322	EST - M14123_apt	EST - M14123_apt	EST - M14123_apt	EST - M14123_apt	
2315	85	M14123	Hs 17731	ESTs	Hs 17731	ESTs	
37253	85	AA449357	Hs 101234	ESTs	Hs 101234	ESTs	
39874	85	T40838	Hs 8330	ESTs	Hs 8330	ESTs	
22313	85	T40838	Hs 2184	Connective tissue activation peptide III	Hs 2184	Connective tissue activation peptide III	
2798	85	M54985	Hs 75188	WEE1-LIKE PROTEIN KINASE	Hs 75188	WEE1-LIKE PROTEIN KINASE	
32479	84	H08701	Hs 27846	ESTs	Hs 27846	ESTs	Weakly similar to RHONBINOTIN-1 [H: sapiens]
16081	84	R03545	Hs 18930	ESTs	Hs 18930	ESTs	
21098	83	D15894	Hs 34782	ESTs	Hs 34782	ESTs	
14733	83	AA447586	Hs 77204	Human CENP-F kinetochore protein mRNA complete cds	Hs 77204	Human CENP-F kinetochore protein mRNA complete cds	
37154	83	AA313387	Hs 133101	ESTs	Hs 133101	ESTs	Highly similar to HYPOTHETICAL 84.7 KD PROTEIN ZK1098.1 IN CHROMOSOME III [Caenorhabditis elegans]
8068	83	AA179547	Hs 81598	ESTs	Hs 81598	ESTs	
7463	83	AA039868	Hs 81420	ESTs	Hs 81420	ESTs	
16501	82	AA039868	Hs 10420	ESTs	Hs 10420	ESTs	
34527	82	U13847	Hs 38442	Human mRNA for Pmi-1 isoform 1	Hs 38442	Human mRNA for Pmi-1 isoform 1	
6100	82	H45840	Hs 81278	Human 75-KD antigen (PM-Sc1) mRNA complete cds	Hs 81278	Human 75-KD antigen (PM-Sc1) mRNA complete cds	
2632	82	AA172372	Hs 26508	ESTs	Hs 26508	ESTs	
11188	82	T93333	Hs 127730	ESTs	Hs 127730	ESTs	Weakly similar to coded for C. elegans cDNA Y4110g.3 [C: elegans]
42293	82	T03330	Hs 2246	Human (gamma) globulin cell line protein 10 from	Hs 2246	Human (gamma) globulin cell line protein 10 from	
3443	82	T03330	EST - RC_189505	EST - RC_189505	EST - RC_189505	EST - RC_189505	
23371	81	T03330	Hs 87702	ESTs	Hs 87702	ESTs	
17306	81	AA086201	Hs 65825	ESTs	Hs 65825	ESTs	
18497	81	AA231795	Hs 149533	Human mRNA for KIAA0018 gene complete cds	Hs 149533	Human mRNA for KIAA0018 gene complete cds	
235	81	D13844	Hs 118335	ESTs	Hs 118335	ESTs	
24523	81	Z13547	EST - AA248884	EST - AA248884	EST - AA248884	EST - AA248884	
7626	81	R33715	Hs 123918	Human sapiens clone 21540 mRNA sequence	Hs 123918	Human sapiens clone 21540 mRNA sequence	
32142	81	AA620465	Hs 112880	ESTs	Hs 112880	ESTs	
39087	80	X78116	Hs 31355	Caenorhabditis alpha S1	Hs 31355	Caenorhabditis alpha S1	
6235	80	AA620465	Hs 41116	ESTs	Hs 41116	ESTs	
28517	80	AA620465	Hs 16822	ESTs	Hs 16822	ESTs	Moderately similar to subunit factor eIF-2B gamma subunit [R: noneglect]
39344	79	C21034					

## FIGURE 4 (CONT.)

18931	76	Hs 20889	ESTs	Hs 20889	ESTs	Hs 20889	ESTs	Hs 20889	ESTs
18933	77	Hs 24227	ESTs	Hs 24227	ESTs	Hs 24227	ESTs	Hs 24227	ESTs
18936	78	Hs 80057	ESTs	Hs 80057	ESTs	Hs 80057	ESTs	Hs 80057	ESTs
36023	79	Hs 97363	ESTs	Hs 97363	ESTs	Hs 97363	ESTs	Hs 97363	ESTs
2192	78	Hs 20954	Human Sapiens angiotensin II receptor gene complete cds	Hs 20954	Human Sapiens angiotensin II receptor gene complete cds	Hs 20954	Human Sapiens angiotensin II receptor gene complete cds	Hs 20954	Human Sapiens angiotensin II receptor gene complete cds
33016	74	L48211	Hs 41716	Hs 41716	Hs 41716	Hs 41716	Hs 41716	Hs 41716	Hs 41716
40014	77	Hs 99291	ESTs	Hs 99291	ESTs	Hs 99291	ESTs	Hs 99291	ESTs
36295	77	Hs 98415	ESTs	Hs 98415	ESTs	Hs 98415	ESTs	Hs 98415	ESTs
19564	77	Hs 32836	ESTs	Hs 32836	ESTs	Hs 32836	ESTs	Hs 32836	ESTs
18914	77	Hs 23744	ESTs	Hs 23744	ESTs	Hs 23744	ESTs	Hs 23744	ESTs
35967	76	Hs 6891	Human splicing factor SRO55-2 (SRSF5) mRNA complete cds	Hs 6891	Human splicing factor SRO55-2 (SRSF5) mRNA complete cds	Hs 6891	Human splicing factor SRO55-2 (SRSF5) mRNA complete cds	Hs 6891	Human splicing factor SRO55-2 (SRSF5) mRNA complete cds
21872	76	Hs 12328	ESTs	Hs 12328	ESTs	Hs 12328	ESTs	Hs 12328	ESTs
19918	76	Hs 14699	ESTs	Hs 14699	ESTs	Hs 14699	ESTs	Hs 14699	ESTs
17721	76	Hs 71711	ESTs	Hs 71711	ESTs	Hs 71711	ESTs	Hs 71711	ESTs
26134	76	Hs 87694	ESTs	Hs 87694	ESTs	Hs 87694	ESTs	Hs 87694	ESTs
18796	76	Hs 12755	ESTs	Hs 12755	ESTs	Hs 12755	ESTs	Hs 12755	ESTs
34492	75	Hs 96	ATL-deficient DNA-dependent (APR) protease	Hs 96	ATL-deficient DNA-dependent (APR) protease	Hs 96	ATL-deficient DNA-dependent (APR) protease	Hs 96	ATL-deficient DNA-dependent (APR) protease
35975	74	Hs 3498	ESTs	Hs 3498	ESTs	Hs 3498	ESTs	Hs 3498	ESTs
29942	74	Hs 43050	ESTs	Hs 43050	ESTs	Hs 43050	ESTs	Hs 43050	ESTs
5793	74	Hs 83759	CDC28 protein kinase 2	Hs 83759	CDC28 protein kinase 2	Hs 83759	CDC28 protein kinase 2	Hs 83759	CDC28 protein kinase 2
31571	74	Hs 50004	ESTs	Hs 50004	ESTs	Hs 50004	ESTs	Hs 50004	ESTs
23763	74	Hs 15053	ESTs	Hs 15053	ESTs	Hs 15053	ESTs	Hs 15053	ESTs
35103	73	Hs 97113	EST	Hs 97113	EST	Hs 97113	EST	Hs 97113	EST
34732	73	Hs 105234	ESTs	Hs 105234	ESTs	Hs 105234	ESTs	Hs 105234	ESTs
29216	73	Hs 134943	ESTs	Hs 134943	ESTs	Hs 134943	ESTs	Hs 134943	ESTs
29418	72	Hs 103159	ESTs	Hs 103159	ESTs	Hs 103159	ESTs	Hs 103159	ESTs
42504	72	Hs 78033	Hs 78033	Hs 78033	Hs 78033	Hs 78033	Hs 78033	Hs 78033	Hs 78033
8111	72	Hs 26170	ESTs	Hs 26170	ESTs	Hs 26170	ESTs	Hs 26170	ESTs
41773	72	Hs 39328	ESTs	Hs 39328	ESTs	Hs 39328	ESTs	Hs 39328	ESTs
9951	71	Hs 9491	ESTs	Hs 9491	ESTs	Hs 9491	ESTs	Hs 9491	ESTs
28109	71	Hs 124315	ESTs	Hs 124315	ESTs	Hs 124315	ESTs	Hs 124315	ESTs
980	71	Hs 124025	ESTs	Hs 124025	ESTs	Hs 124025	ESTs	Hs 124025	ESTs
29648	71	Hs 129445	ESTs	Hs 129445	ESTs	Hs 129445	ESTs	Hs 129445	ESTs
30528	71	Hs 112013	ESTs	Hs 112013	ESTs	Hs 112013	ESTs	Hs 112013	ESTs
22547	70	Hs 20474	ESTs	Hs 20474	ESTs	Hs 20474	ESTs	Hs 20474	ESTs
9347	70	Hs 102520	EST	Hs 102520	EST	Hs 102520	EST	Hs 102520	EST
11896	70	Hs 137555	PROBABLE G PROTEIN-COUPLED RECEPTOR HN74	Hs 137555	PROBABLE G PROTEIN-COUPLED RECEPTOR HN74	Hs 137555	PROBABLE G PROTEIN-COUPLED RECEPTOR HN74	Hs 137555	PROBABLE G PROTEIN-COUPLED RECEPTOR HN74
40584	70	Hs 259	Colipase	Hs 259	Colipase	Hs 259	Colipase	Hs 259	Colipase
193	70	Hs 48876	FARNESYL-ORPHOSPHATE FARNESYL TRANSFERASE	Hs 48876	FARNESYL-ORPHOSPHATE FARNESYL TRANSFERASE	Hs 48876	FARNESYL-ORPHOSPHATE FARNESYL TRANSFERASE	Hs 48876	FARNESYL-ORPHOSPHATE FARNESYL TRANSFERASE
13305	70	Hs 89113	ESTs	Hs 89113	ESTs	Hs 89113	ESTs	Hs 89113	ESTs
8078	70	Hs 67007	EST	Hs 67007	EST	Hs 67007	EST	Hs 67007	EST
26741	69	Hs 12066	ESTs	Hs 12066	ESTs	Hs 12066	ESTs	Hs 12066	ESTs
35269	68	Hs 37286	Human Sapiens orphan nuclear hormone receptor DD73 mRNA 3' end	Hs 37286	Human Sapiens orphan nuclear hormone receptor DD73 mRNA 3' end	Hs 37286	Human Sapiens orphan nuclear hormone receptor DD73 mRNA 3' end	Hs 37286	Human Sapiens orphan nuclear hormone receptor DD73 mRNA 3' end
23504	68	Hs 105299	ESTs	Hs 105299	ESTs	Hs 105299	ESTs	Hs 105299	ESTs
799	68	Hs 11732	ACETATE OXIDOREDUCTASE	Hs 11732	ACETATE OXIDOREDUCTASE	Hs 11732	ACETATE OXIDOREDUCTASE	Hs 11732	ACETATE OXIDOREDUCTASE
40583	68	Hs 11429	ESTs	Hs 11429	ESTs	Hs 11429	ESTs	Hs 11429	ESTs
31934	68	Hs 88494	Test (Osteopontin) home box homolog 2	Hs 88494	Test (Osteopontin) home box homolog 2	Hs 88494	Test (Osteopontin) home box homolog 2	Hs 88494	Test (Osteopontin) home box homolog 2
24578	68	Hs 12287	ESTs	Hs 12287	ESTs	Hs 12287	ESTs	Hs 12287	ESTs
8376	68	Hs 81791	Human Sapiens mRNA for osteosarcoma embryonic factor (OCF) complete cds	Hs 81791	Human Sapiens mRNA for osteosarcoma embryonic factor (OCF) complete cds	Hs 81791	Human Sapiens mRNA for osteosarcoma embryonic factor (OCF) complete cds	Hs 81791	Human Sapiens mRNA for osteosarcoma embryonic factor (OCF) complete cds
19186	68	Hs 34602	ESTs	Hs 34602	ESTs	Hs 34602	ESTs	Hs 34602	ESTs
15486	67	Hs 1044	CTTCCHROME P4-50 VII	Hs 1044	CTTCCHROME P4-50 VII	Hs 1044	CTTCCHROME P4-50 VII	Hs 1044	CTTCCHROME P4-50 VII
25675	67	Hs 23130	ESTs	Hs 23130	ESTs	Hs 23130	ESTs	Hs 23130	ESTs
5844	67	Hs 23130	ESTs	Hs 23130	ESTs	Hs 23130	ESTs	Hs 23130	ESTs
13881	66	Hs 23130	ESTs	Hs 23130	ESTs	Hs 23130	ESTs	Hs 23130	ESTs

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**FIGURE 4 (CONT.)**

22194	Q09596	Hs	42496	EST1	
33333	KJ0910	Hs	Z32650	Oxydn B1	
33333	L33695	Hs	Z32650	Nuclear factor of kappa light polypeptide gene enhancer in b-cells 2 (c-Rel-p100)	
33333	N08184	Hs	B15154	EST5	
33333	V052000	Hs	B15155	Home sapiens clone 24433 mRNA sequence	
33333	Hs	B15155	Home sapiens clone 24433 mRNA sequence		
33333	Hs	B756	EST5	Weakly similar to PROBABLE E3 PROTEIN [human papillomavirus type 58]	
33333	Hs	B10533	EST5		
33333	V051900	Hs	B10533	EST5	
33333	F10243	Hs	B0873	EST5	Weakly similar to IIII ALL CLASS B WARMING ENTRY int [H sapiens]
33333	C14083	Hs	B73300	EST4	
33333	A4423346	Hs	B69306	EST4	
33333	M27015	Hs	B18457	EST5	
33333	Hs	B2783	RETINOIC ACID RECEPTOR BETA-2		
33333	A4428633	Hs	B98004	EST	
33333	Y02091	Hs	B24912	Home sapiens bicucullin-D (BICD) mRNA complete cds	
33333	Hs	B7552	EST		
33333	A4451894	Hs	B89744	EST	
33333	A4007147	Hs	B59552	EST	
33333	S59798	Hs	B18917	EST5	
33333	A4417740	Hs	B95345	EST5	
33333	V07693	Hs	B55000	EST5	
33333	A4180448	Hs	B143000	EST	
33333	A4486073	Hs	B37363	EST5	
33333	A4454747	Hs	B14504	EST5	
33333	X95913	Hs	B755	Integrin alpha 2b (platelet glycoprotein IIb or fibrin complex antigen CD41B)	
33333	T30272	Hs	B2704	Guaninephosphatase 2 gastrinreceptor	
33333	T17063	Hs	B4220	EST5	Weakly similar to tetacycline transposase-like protein [M musculus]
33333	A4068459	Hs	B19522	EST5	Weakly similar to IIII ALL SUBFAMILY J WARMING ENTRY int [H sapiens]
33333	A4657295	Hs	B69621	EST5	
33333	Hs	B1308	Hs	B40253	EST
33333	R44536	Hs	B140889	EST5	
33333	F10927	Hs	B65183	Home sapiens clone Z9355 mRNA sequence	
33333	A4178445	Hs	B73623	EST5	Moderately similar to rabiesvirus G [M musculus]
33333	R55995	Hs	B142077	EST5	
33333	A45004307	Hs	B96284	X-LINKED HELICASE II	
33333	D30007	Hs	B45028	Human mRNA for KIAA0185 gene partial cds	
33333	U23182	Hs	B83363	Human endonuclease AOC37-2 mRNA complete cds	
33333	HQ33546-HT37344	Hs	EST - HQ3546-HT3744		
33333	T10249	Hs	B4780	EST5	
33333	A4435524	Hs	B97483	EST	
33333	L40284	Hs	EST - L40284		
33333	A4251137	Hs	B109270	EST5	
33333	X58206	Hs	EST - X58206_cds2		
33333	Z30612	Hs	B144000	EST5	
33333	C31116	Hs	B84541	EST5	
33333	A4211801	Hs	B86430	EST5	
33333	U91327	Hs	EST - U91327		
33333	M26167	Hs	B72953	Human platelet factor 4 version 1 (PF4v1) gene complete cds	
33333	A4494795	Hs	EST - RC_AA481745		
33333	U33386	Hs	B90073	Human chromosome segregation gene homolog CAS mRNA complete cds	
33333	U16981	Hs	B2133	Retinal pigment epithelium-specific protein (RSP4)	
33333	Z39201	Hs	B7259	EST5	
33333	Z46679	Hs	B2316	SRV (var-determining region V)-box 5 (camponotric cytoplasmic autosomal sea-reversal)	
33333	A4060793	Hs	B136663	EST5	
33333	C14573	Hs	B75393	Human mRNA for KIAA0079 gene partial cds	
33333	A4232231	Hs	B24596	EST - X62279	
33333	G62279	Hs	EST - X62279		

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## FIGURE 4 (CONT.)

2645	M25753	Hs 23860	Cylin B1
3392	M93127	Hs 59422	ESTs
2843	D60252	Hs 113619	ESTs
6160	X74794	Hs 89509	CD21 HOMOLOG
42515	U72116	Hs 100333	Homo sapiens clone 23822 mRNA sequence
4732	U58372	Hs 84713	Human huntingtin interacting protein (HHP2) mRNA complete cds
3299	M95023	Hs 82609	Hydroxymethylglutaryl synthase
28320	AA399574	Hs 65370	ESTs
745	D84454	Hs 21899	Human mRNA for UTP-glucose translocator complete cds
3117	M81182	Hs 78181	Precortical membrane protein 1 (POMP) (Zebrafish syndrome)
21257	R09196	Hs 20221	ESTs Moderately similar to M-phase phosphoprotein 11 (p11)
31407	N95207	Hs 128849	ESTs
29554	F03153	Hs 80383	ESTs
39728	AA605955	Hs 109960	ESTs
29903	N23366	Hs 83364	EST
9470	AA481250	Hs 54590	ESTs
28209	H46617	EST - H46617	
9435	M00201	EST - H30201	
27411	AA428137	Hs 86434	ESTs
30515	N50556	Hs 47076	ESTs
29954	N24194	Hs 43331	ESTs
1064	AA186904	EST - H32846-H72953	
11232	AA287450	Hs 25740	ESTs Weakly similar to unknown (S. cerevisiae)
26643	AA305116	Hs 83642	ESTs
8035	H15054	Hs 22164	ESTs
19263	Z38810	Hs 27194	ESTs
24586	C21245	Hs 11171	M sapiens mRNA for apocaps specific protein
28559	X17096	Hs 108938	Pregnancy-specific beta-1 glycoprotein 6
5664	N51781	Hs 47338	EST
30710	AA256490	Hs 44610	ESTs
20360	M15796	Hs 78596	Proliferating cell nuclear antigen
2351	N35065	Hs 44590	Homo sapiens clone 24739 mRNA sequence
30262	T03886	Hs 100265	ESTs
41792	AA434411	Hs 86505	ESTs
38710	F09134	Hs 111803	ESTs
42165	T79551	Hs 12639	ESTs
18745	AA406093	Hs 86178	M sapiens mRNA for M-phase phosphoprotein ppp9
35748	AA433328	Hs 12544	ESTs
27595	AA433328	Hs 12544	ESTs
39900	AA433328	Hs 12544	ESTs
21117	AA433328	Hs 12544	ESTs
33458	AA433328	Hs 12544	ESTs
26663	AA433328	Hs 12544	ESTs
12689	AA417030	Hs 5101	Homo sapiens protein regulating cytolysis 1 (PRC1) mRNA complete cds
29701	H97870	Hs 42478	EST
34428	AA392436	Hs 27821	Homo sapiens semaphorin F homolog mRNA complete cds
14865	U15128	Hs 36573	Human beta-12 N-acetylglucosaminyltransferase II (MGAT2) gene complete cds
34761	AA287833	Hs 89608	ESTs
23211	T40859	Hs 83329	ESTs
40811	N39138	Hs 100784	Homo sapiens mRNA for KIAA0564 protein partial cds
42611	W87006	Hs 79440	Homo sapiens putative RNA binding protein KOC (KOC) mRNA complete cds
17581	AA129395	Hs 71139	EST
18712	F04677	Hs 12381	ESTs
30709	N51754	Hs 47334	ESTs Weakly similar to synapse-associated protein 96A7-1 (D. melanogaster)
34179	AA227903	Hs 41127	ESTs Highly similar to GTP-BINDING PROTEIN LEPA (Pseudomonas fluorescens)
1265	HG4157-H74427	EST - HG4157-H74427	

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## FIGURE 4 (CONT.)

1106	HC2981: HT3127	EST - HC2981: HT3127	Hs 40323 Homo sapiens spleen mitotic checkpoint BUD3 (BUD3) mRNA complete cds
34367	AA251756	Hs 8504 ESTs	
34802	AA291468	Hs 8504 ESTs	
11595	AA242819	Hs 125014 ESTs	
8295	AA405082	Hs 125014 ESTs	
17622	AA131584	Hs 71432 ESTs Weakly similar to SOF1 PROTEIN (Saccharomyces cerevisiae)	
34754	AA297642	Hs 81844 Human mRNA for KIAA0076 gene complete cds	
37687	AA460310	Hs 110165 ESTs Highly similar to 60S RIBOSOMAL PROTEIN L26 (Rattus norvegicus)	
38072	AA458987	Hs 141982 ESTs	
25038	AA010065	Hs 83728 CDC28 protein kinase 2	
32503	117045	Hs 80733 Collagen type I alpha 2	
3270	M94025	Hs 54498 SODIUM CHANNEL PROTEIN BRAIN II ALPHA SUBUNIT	
9996	L38961	Hs 85459 Integral transmembrane protein 1	
36387	AA176270	Hs 84348 ESTs	
31381	N87869	Hs 49387 ESTs	
29723	AA262781	Hs 95311 ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP28 (Saccharomyces cerevisiae)	
36296	AA489647	Hs 49624 ESTs	
14474	AA609427	Hs 120119 ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (Nucleobus coucang)	
5312	L90716	Hs 79184 ESTs Moderately similar to III ALU SUBFAMILY SC WARNING ENTRY III (H. sapiens)	
34581	AA401750	Hs 79187 Human cell surface protein HCAR mRNA complete cds	
29739	H99436	Hs 97343 EST	
7203	AA023096	Hs 42710 EST	
2157	L11519	Hs 83403 Homo sapiens protein-tyrosine kinase EphA2v (EPH2) mRNA complete cds	
8045	AA134778	Hs 52954 ESTs	
33656	D13633	Hs 105484 ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR (H. sapiens)	
34065	W62477	Hs 77895 Human mRNA for KIAA0008 gene complete cds	
8028	AA195517	Hs 50582 ESTs	
4126	U29463	Hs 111180 ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III (H. sapiens)	
41099	N93969	Hs 90011 Adenylsuccinate synthase	
8264	AA401334	Hs 108102 Cytochrome B561	
27558	AA443187	Hs 81107 H. sapiens mRNA for NF-ai protein	
34478	Y13045	Hs 109541 ESTs	
11270	AA193399	Hs 41181 ESTs	
39222	AA651348	Hs 122578 ESTs	
7658	AA451188	Hs 110736 Human homonucleotide sensitive Na,K-ATPase (HsCC1) mRNA complete cds	
19902	AA453082	Hs 74641 ESTs	
10316	AA453319	Hs 50922 Homo sapiens mRNA for nuclear protein Nhp59	
13193	AA442783	Hs 110042 ESTs Highly similar to DOLICHYL PHOSPHATE BETA-GLUCOSYL TRANSFERASE (Saccharomyces cerevisiae)	
4693	AA118720	Hs 82273 ESTs	
31683	AA118720	Hs 81454 ESTs	
78131	AA609712	Hs 34190 ESTs	
33548	AA609712	Hs 9951 ESTs	
38300	AA609712	Hs 20483 ESTs Highly similar to G2M1TIC-SPECIFIC CYCLIN B2 (Macrodolus auratus)	
38106	AA609712	Hs 114938 NUCLEOSIDE DIPHOSPHATE KINASE A	
38930	AA609712	Hs 72782 ESTs	
10251	AA609712	Hs 59492 ESTs	
31638	AA609712	Hs 82453 EST	
1572	AA609712	Hs 71049 ESTs	
		Hs 39972 ESTs Weakly similar to transcription LPE2 reverse transcriptase homolog (H. sapiens)	
		Hs 110462 ESTs	
		Hs 111482 ESTs	
		Hs 28558 ESTs Moderately similar to III ALU SUBFAMILY SO WARNING ENTRY III (H. sapiens)	
		Hs 18171 ESTs Weakly similar to CD148.7 (C. elegans)	
		Hs 57435 Natural resistance-associated macrophage protein 2	
		EST - R01864	

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## FIGURE 4 (CONT.)

10923	4.2	AA116036	Hs.9229	ESTs	
34360	4.2	AA252414	Hs.104300	ESTs	
10112	4.2	R35733	EST - R35733		
10829	4.2	AA038811	Hs.61559	ESTs	
23146	4.2	AA026356	Hs.106106	ESTs	
23146	4.2	D20959	Hs.3656	ESTs Moderately similar to an ALU SUBFAMILY SO WARNING ENTRY 99 [H sapiens]	
10200	4.2	R64321	Hs.77361	ESTs	
36695	4.2	AA000176	Hs.112245	ESTs	
31365	4.2	AA000176	Hs.48907	ESTs	
42378	4.2	V07189	Hs.100018	ESTs	
28050	4.1	AA479139	Hs.73393	Acid phosphatase 1 soluble	
2820	4.1	M29474	Hs.73558	Human recombination activating protein (RAG-1) gene complete cds	
8927	4.1	AF008442	Hs.5409	Homo sapiens RNA polymerase I subunit RPL39 mRNA complete cds	
13379	4.1	AA449741	Hs.4029	ESTs Weakly similar to AF-9 PROTEIN [H sapiens]	
5134	4.1	U79523	Hs.80802	Human clone 23948 mRNA sequence	
36575	4.1	AA431085	Hs.98706	EST	
143	4.1	HUMTFRM11507			
10970	4.1	AA129390	Hs.5285	ESTs	AFEX-HUMTFRM11507_5
25838	4.1	AA152365	Hs.2248	Interferon (gamma)-induced cell line protein 10 from	
19735	4.1	H53038	Hs.26710	EST	
40711	4.1	N53364	Hs.106156	ESTs	
4149	4.1	U26386	Hs.2387	RAG (recombination activating gene) cohort 1	
5767	4.1	X53793	Hs.116226	MULTIFUNCTIONAL PROTEIN ADE2	
5503	4.1	X05232	Hs.83326	Stoneysen	
23310	4.1	N34593	Hs.61553	ESTs Highly similar to HYPOTHETICAL 47.8 KD PROTEIN B0200.9 IN CHROMOSOME II [Caenorhabditis elegans]	
456	4.1	D38145	Hs.61333	Prostaglandin G/H synthase	
33651	4.0	V65409	Hs.59704	ESTs	
19110	4.0	H08778	Hs.133521	ESTs	
24408	4.0	V00146	Hs.25982	ESTs	
26598	4.0	AA279943	Hs.80671	ESTs	
32969	4.0	V42451	Hs.82290	ESTs	
27006	4.0	AA398695	Hs.56159	ESTs Weakly similar to EMF2 gene product [C. elegans]	
29609	4.0	N21043	Hs.42932	EST	
9598	3.8	H91564	Hs.13540	ESTs	
29024	3.8	F09315	Hs.76982	Homo sapiens mRNA for KIA0583 protein partial cds	
21684	3.8	R39317	Hs.89403	Homo sapiens protein-tyrosine kinase EphA2 (EPH2) mRNA complete cds	
37863	3.8	AA478823	Hs.89619	ESTs Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A1.04C [Schistosoma mansoni]	
6961	3.8	HUMTFRM11507			
24882	3.8	Z41415	Hs.0623	ESTs Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]	
26685	3.8	AA261550	Hs.79656	ESTs	
42300	3.8	T54590	Hs.100703	ESTs	
6495	3.8	X82715	Hs.3057	Zinc finger protein 74 (Cez52)	
38604	3.8	AA358803	Hs.111496	ESTs	
30560	3.8	N49264	Hs.1334	MYB PROTO-ONCOGENE PROTEIN	
14413	3.8	AA000150	Hs.14368	ESTs	
38156	3.8	AA487021	Hs.105709	EST	
2572	3.8	M27281	Hs.73793	Vascular endothelial growth factor	
40100	3.8	H75933	Hs.75901	Lemnin receptor (RH5 epitope)	
20944	3.8	N74443	Hs.16247	ESTs	
8513	3.8	AA468990	Hs.103135	ESTs	
13877	3.8	AA476504	Hs.7114	ESTs	
14509	3.8	AA609943	Hs.32793	ESTs	
10281	3.8	R80333	Hs.21182	ESTs	
23284	3.8	AA045074	Hs.110146	ESTs Weakly similar to S2-MD SS-A/Ro autoantigen [H sapiens]	
6730	3.8	Y05305	Hs.17154	H.sapiens mRNA for protein kinase Dyrk4 partial	
18033	3.8	HUMSGF3A49783			AFEX-HUMSGF3A49783_1MB

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## FIGURE 4 (CONT.)

39742	A4621523	Hs.110832	ESTs	Hs.100115	Human mRNA for KIAA0007 gene partial cds
27354	A442521	Hs.81688	ESTs	Hs.50473	ESTs
4532	U49188	Hs.75326	Human placenta (CHD3) mRNA complete cds	Hs.35828	ESTs
18395	A427219	Hs.110828	Human testis CAGP9 mRNA partial cds	Hs.110406	ESTs
16754	A404697	EST - RC_A404697		Hs.84891	ESTs
42463	U60190	Hs.100115	Human mRNA for KIAA0007 gene partial cds	Hs.771622	ESTs
867	D87716	Hs.100115	Human mRNA for KIAA0007 gene partial cds	Hs.1197	Heat shock 10 KD protein 1 (chaperonin 10)
31795	H80703	Hs.50473	ESTs	Hs.111758	KERATIN TYPE II CYTOSKELETAL 60
22828	R88192	Hs.35828	ESTs	Hs.82321	Human RNA binding protein EL-3 mRNA complete cds
25240	A4039713	Hs.110406	ESTs	Hs.32170	ESTs
4341	U38545	Hs.84891	ESTs	Hs.75687	Human testis cytochrome P-450 mRNA complete cds
17463	A112147	Hs.771622	ESTs	Hs.125386	ESTs
18654	A053532	Hs.1197	Heat shock 10 KD protein 1 (chaperonin 10)	Hs.94781	ESTs
3709	U07550	Hs.111758	KERATIN TYPE II CYTOSKELETAL 60	Hs.21201	ESTs
1608	U02005	Hs.82321	Human RNA binding protein EL-3 mRNA complete cds	Hs.13886	Human testis importin- $\alpha$ homolog (SRP19) mRNA complete cds
4951	U09548	Hs.32170	ESTs	Hs.134510	Human HIV-1 late element modulatory factor mRNA sequence from chromosome 3
20418	N49209	Hs.75687	Human testis cytochrome P-450 mRNA complete cds	Hs.13885	ESTs
27995	A4470155	Hs.125386	ESTs	Hs.16056	ESTs
7971	A4387423	Hs.94781	ESTs	Hs.78494	Human testis mRNA for KIAA0525 protein partial cds
27008	A443793	Hs.21201	ESTs	Hs.28448	ESTs
24877	Z39336	Hs.13886	Human testis importin- $\alpha$ homolog (SRP19) mRNA complete cds	Hs.62386	ESTs
9328	D89618	Hs.134510	Human HIV-1 late element modulatory factor mRNA sequence from chromosome 3	Hs.111710	ESTs
17878	A1134275	Hs.13885	ESTs	Hs.1846	Tumor protein p53 (Li-Fraumeni syndrome)
36709	A4421266	Hs.16056	ESTs	Hs.107147	ESTs
20084	H88653	Hs.78494	Human testis mRNA for KIAA0525 protein partial cds	Hs.54849	Hs.54849
9713	L44338	Hs.28448	ESTs	Hs.20396	ESTs
28622	D11837	Hs.62386	ESTs	EST - RC_T06595	
26628	D11888	Hs.111710	ESTs	Hs.2012	TRANSCOBALAMIN I PRECURSOR
25804	A1148935	Hs.1846	Tumor protein p53 (Li-Fraumeni syndrome)	Hs.94590	ESTs
2492	M72899	Hs.107147	ESTs	Hs.3823	INITIATION FACTOR IF-2 MITOCHONDRIAL PRECURSOR
14904	A043765	Hs.54849	Hs.54849	Hs.2359	Human MAP kinase phosphatase (MKP-2) mRNA complete cds
25205	A4456437	Hs.20396	ESTs	Hs.3281	Neuronal pentosan II
13068	T98395	EST - RC_T06595		EST - RC_A403070_s	
42307	J05069	Hs.2012	TRANSCOBALAMIN I PRECURSOR	Hs.18528	ESTs
1544	197257	Hs.94590	ESTs	Hs.98117	ESTs
42311	L34600	Hs.3823	INITIATION FACTOR IF-2 MITOCHONDRIAL PRECURSOR	Hs.5101	Human testis protein regulating cyclinase 1 (PRC1) mRNA complete cds
2023	U48807	Hs.2359	Human MAP kinase phosphatase (MKP-2) mRNA complete cds	EST - Q25589	
4540	Z39287	Hs.3281	Neuronal pentosan II	Hs.20890	ESTs
33707	A403070	EST - RC_A403070_s		Hs.27437	ESTs
17220	V85782	Hs.18528	ESTs	Hs.33748	ESTs
24332	A4412087	Hs.98117	ESTs	Hs.1191	Human mRNA for KIAA0073 gene partial cds
35887	A4417132	Hs.5101	Human testis protein regulating cyclinase 1 (PRC1) mRNA complete cds	Hs.34045	ESTs
8336	D18589	Hs.20890	ESTs	Hs.107932	Hs.107932
387	A4398109	Hs.27437	ESTs	Hs.72614	Human high-affinity copper uptake protein (HCTR1) mRNA complete cds
12319	V85047	Hs.33748	ESTs	Hs.84728	Basic transcription element binding protein 2
15843	A1190458	Hs.1191	Human mRNA for KIAA0073 gene partial cds	Hs.363	Zinc finger protein 139 (clone pHL37)
11218	A4029328	Hs.34045	ESTs	Hs.8053	ESTs
16539	H28581	Hs.107932	Hs.107932	Hs.39441	ESTs
29203	A4465342	Hs.72614	Human high-affinity copper uptake protein (HCTR1) mRNA complete cds		
13638	A1112258	Hs.84728	Basic transcription element binding protein 2		
25585	A1191488	Hs.363	Zinc finger protein 139 (clone pHL37)		
34016	D14520	Hs.8053	ESTs		
251	U09848	Hs.39441	ESTs		
3778	Z38409				
24535					
18127					

## FIGURE 4 (CONT.)

Hs.60476	ESTs: Weakly similar to ZINC FINGER PROTEIN 91 [H. sapiens]
Hs.3280	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA complete cds
Hs.37781	NAQ-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE
Hs.47232	ESTs
Hs.06385	ESTs
Hs.98493	DNA-REPAIR PROTEIN XRCC1
Hs.69900	ESTs
Hs.74284	ESTs: Moderately similar to Similar to S. cerevisiae hypophosphorylated protein L3111 [H. sapiens]
Hs.44045	ESTs
Hs.43133	Homo sapiens mRNA for KIAA0828 protein complete cds
Hs.81690	Homo sapiens importin beta subunit mRNA complete cds
Hs.24837	Homo sapiens sodium/myosin-coupled cotransporter (SLC5A3) gene complete cds
Hs.756	ESTs
Hs.97332	ESTs: Moderately similar to ovalbumin-specific protein [R. norvegicus]
Hs.87339	ESTs: Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN PM16-PC11 INTERGENIC REGION [Saccharomyces cerevisiae]
Hs.8104	ESTs
Hs.31838	ESTs
Hs.24595	EST
Hs.119387	ESTs
Hs.75601	Human FX protein mRNA complete cds
Hs.17286	ESTs
EST - RC_AA070364	
Hs.44131	ESTs
Hs.80081	ESTs
Hs.35682	Human translation initiation factor eIF3 p66 subunit mRNA complete cds
Hs.12475	Homo sapiens clone Z6817 unknown mRNA partial cds
Hs.50722	Human mRNA for KIAA0334 gene complete cds
Hs.31748	H. sapiens mRNA for TRES
EST - L41390	
Hs.39454	ESTs: Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]
ATFX-HUNTERRAM1507_M	
Hs.91379	PTB-ASSOCIATED SPLICING FACTOR
Hs.87157	130 KD LEUCINE-RICH PROTEIN
Hs.5172	Human Oa protein mRNA partial cds
Hs.21726	ESTs
Hs.24287	ESTs
Hs.125123	ESTs: Weakly similar to H. ALU SUBFAMILY J WARNING ENTRY [H. sapiens]
Hs.46495	EST
Hs.21043	ESTs
Hs.6347	ESTs
Hs.42179	ESTs
Hs.54174	ESTs
Hs.25916	ESTs
Hs.87982	Thymidylate synthase
Hs.48915	Homo sapiens ornithine decarboxylase (BDX) mRNA complete cds
Hs.36708	Homo sapiens MAC2-like protein kinase mRNA complete cds
Hs.12338	ESTs
Hs.69149	ESTs
Hs.103048	ESTs
Hs.63220	ESTs: Weakly similar to GA BINDING PROTEIN BETA 2 CHAIN [H. sapiens]
Hs.131381	PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT TESTIS-SPECIFIC FORM PRECURSOR
Hs.48269	Homo sapiens mRNA for VRK1 complete cds
Hs.15140	ESTs
Hs.3566	ESTs: Highly similar to phosphorylation regulatory protein p34 [R. norvegicus]
Hs.106635	ESTs: Weakly similar to T23511.7 [C. elegans]
Hs.5337	ESTs: Highly similar to ribosome-binding protein p34 [R. norvegicus]

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## FIGURE 4 (CONT.)

11140	31	AA158132	Hs.11817 EST highly similar to YSA1 PROTEIN [Schistosoma carolinense]
14372	31	AA161068	Hs.21693 EST highly similar to PROBABLE PEPTIDYL-PROLYL CYSTEINE ISOMERASE C21E11.02 [Schistosoma carolinense]
15096	31	Z114201	Hs.30819 ESTs
17229	30	AA413111	Hs.23393 ESTs
32315	30	AA414036	Hs.38797 ESTs
32929	30	AA414249	Hs.48942 ESTs
17255	30	AA164209	Hs.31730 Homo sapiens RRM RNA binding protein Cry-rip [CRY-RBP] mRNA, complete cds
5083	30	U02992	Hs.71134 Human TAF11 mRNA, complete cds
15060	30	U54999	Hs.93121 Human LON protein mRNA, complete cds
17137	30	AA141224	Hs.71814 EST
25330	30	AA218550	Hs.72731 ESTs
22960	30	T10272	Hs.4267 ESTs
4298	30	U06446	Hs.74374 Human Ca <sup>2+</sup> -dependent activator protein for secretion mRNA, complete cds
7445	30	AA104023	Hs.110048 ESTs
18055	30	AA175937	Hs.73306 ESTs
7282	30	AA083339	Hs.126781 ESTs
806	30	D81009	Hs.43834 Human (lambda) DNA for immunoglobulin light chain
38447	30	AA504255	Hs.34404 Human protein kinase ATR mRNA, complete cds
41464	30	R48937	Hs.107450 ESTs
9662	30	L19161	Hs.121541 TRANSLATIONAL INITIATION FACTOR 2 GANIMA SUBUNIT
13174	30	U82987	Hs.87246 Human Bcl-2 binding component 3 (bcl3) mRNA, partial cds
33620	30	V62943	Hs.95569 ESTs
41077	30	N95026	Hs.125631 ESTs
1932	30	L24804	Hs.75839 Human (p23) mRNA, complete cds
39256	30	F01728	Hs.3657 ESTs
32156	30	R40331	Hs.142852 ESTs
13617	30	AA456646	Hs.20691 ESTs
11949	30	AA261251	Hs.35898 ESTs Weakly similar to ethoxa protein tyrosyl [D melanogaster]
6056	28	X81194	Hs.80918 Pantoic acid (human leucocyte line HsCa1) mRNA, 2105 nt
1605	28	U00056	Hs.79070 V-myc avian myelocytomatous virus oncogene homolog
4536	28	U48705	Hs.75562 Receptor protein-tyrosine kinase EDOR1
10173	28	R56676	Hs.107963 ESTs Weakly similar to cell division control protein CDC21 [H. sapiens]
21009	28	N90431	Hs.28928 ESTs
38200	28	AA421164	Hs.107213 ESTs
33299	28	AA398622	Hs.75133 Transcription factor 6-like 1 (mitochondrial transcription factor 1-like)
9604	28	H74358	Hs.142965 Human SIL mRNA, complete cds
13313	28	AA397916	Hs.22595 ESTs
3928	28	X82046	Hs.75168 WEE1-LIKE PROTEIN KINASE
16189	28	AA195316	Hs.63311 ESTs
19667	28	H61476	Hs.15941 ESTs
6081	28	X69398	Hs.87685 CD47 antigen (Rb-related antigen integrin-associated signal transducer)
3254	28	U87762	Hs.76887 Human 26S proteasome-associated peptidyl homologue (POM1) mRNA, complete cds
13579	28	AA455987	Hs.100705 Human neuronal PAS2 (NPAS2) mRNA, complete cds
38495	28	AA505116	Hs.112355 Human nucleoside diphosphate (NUP88) mRNA, complete cds
2028	28	L35035	Hs.79806 RIBOSE 5-PHOSPHATE ISOMERASE
27374	28	AA425816	Hs.84641 ESTs Weakly similar to Y5C12A.3 [C. elegans]
26106	28	AA243189	Hs.53852 ESTs
4189	28	U01930	Hs.57700 UDP-glucose ceramide glucosyltransferase
16708	28	AA043944	Hs.67893 ESTs
337	28	D28156	Hs.78202 Human mRNA for transcriptional activator hSNF2b, complete cds
26045	28	AA238276	Hs.87267 ESTs
8059	28	AA310967	Hs.5080 ESTs Weakly similar to T0448.1 [C. elegans]
21358	28	R16079	Hs.14775 ESTs
3572	28	S87759	Hs.57764 Protein phosphatase 2C alpha [human testis/carcinoma mRNA, 2346 nt]
11877	28	AA282727	Hs.9591 ESTs
35630	28	AA411448	Hs.135386 ESTs

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## FIGURE 4 (CONT.)

20151	N22955	Hs 6031	Human sapiens data 1400 unknown protein mRNA partial cds
38649	AA592627	EST - RC_AA59267	
7777	AA236820	Hs 18138	EST
32845	V01466	Hs 55459	EST
28258	AA505133	Hs 82223	EST
35944	AA412488	Hs 89150	EST
30948	N50511	Hs 42118	EST
8616	AA460077	Hs 28553	EST
34928	AA342084	EST - RC_AA342084	
328	D21262	Hs 73537	Human mRNA for KIAA0235 gene partial cds
6480	X81786	Hs 84974	H sapiens mRNA for lcn protein
23202	AA034537	Hs 95182	EST
1891	L07493	Hs 15028	Replication protein A (E coli RecA homolog RAD51 homolog)
14568	AA511122	Hs 51168	EST
14182	AA469885	Hs 21768	EST
18253	AA029370	Hs 65248	EST
22511	T03853	Hs 27047	EST
35549	AA403174	Hs 31750	Human sapiens RRM RNA binding protein Gyr-Op (Gyr-RBP) mRNA complete cds
33855	AA412528	Hs 20183	ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH (R norvegicus)
17642	AA132953	Hs 44158	ESTs Moderately similar to C-1-TETRAHYDROQUOLATE SYNTHASE CYTOPLASMIC (H sapiens)
81131	X72841	Hs 21756	Human telomerase-binding protein (RbAp46) mRNA complete cds
41429	AA44004	Hs 108162	ESTs
22937	T110653	Hs 42114	Human sapiens TLS-associated protein TAPR-2 mRNA complete cds
6243	AA012602	Hs 60358	EST
8444	X89750	Hs 90077	H sapiens mRNA for TGF protein
9240	X78627	Hs 75066	H sapiens mRNA for transin
42116	D59924	EST - RC_189924	
7701	AA215333	Hs 97101	EST
17556	AA128605	Hs 22387	EST
42354	V73185	Hs 69403	Human sapiens protein-tyrosine kinase EphA2 (EPH2) mRNA complete cds
28113	N21111	Hs 42948	EST
32173	AA385007	Hs 97381	EST
32583	T27097	Hs 21653	Human mRNA for KIAA0256 gene complete cds
3223	AA443720	Hs 73531	EST
8484	AA443460	Hs 3436	EST
1130	H16937	Hs 819	Human homo box c1 protein mRNA complete cds
2375	F10958	Hs 46571	Human SH3 domain containing protein SH3P18 mRNA complete cds
18958	AA281259	Hs 97101	EST
34786	Z3501	Hs 8188	ESTs Weakly similar to PROBABLE ES PROTEIN (Human papillomavirus type 38)
33688	N52078	Hs 13804	Human sapiens mRNA for KIAA0337 protein complete cds
30733	R09135	Hs 86013	Human sapiens mRNA for KIAA0304 protein partial cds
21256	D82715	Hs 10724	ESTs Weakly similar to unknown (S cerevisiae)
9296	M83712	Hs 18714	Cholinergic receptor nicotinic alpha polypeptide 5
3154	AA093534	Hs 109822	ESTs Weakly similar to HYPOPHYSICAL 18 kD PROTEIN IN SMV2 RPS101 INTERGENIC REGION (S cerevisiae)
7383	L23806	Hs 16955	Neutrophil proteinase 12 (macrophage elastase)
1923	AA459933	Hs 46572	EST
30407	AA753351	Hs 44439	EST
20286	H81487	Hs 17063	EST
9558	AA188901	Hs 85634	EST
18104	AB002359	Hs 105478	Human mRNA for KIAA0261 gene KIAA0261 protein
8863	N49300	Hs 24908	EST
20422	R07258	Hs 59215	ESTs Moderately similar to moctsin (M musculus)
41602	U81601	Hs 79361	Human protease M mRNA complete cds
4821	AA053296	Hs 63138	EST
18807		Hs 20198	ESTs Moderately similar to A8 (R norvegicus)
15289	V07562		

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## FIGURE 4 (CONT.)

23022	10551	26	T91715	Hs 14574	ESTs highly similar to HYPOTHETICAL 103.2 KD PROTEIN IN COX5B-PP2CS INTERGENIC REGION [Saccharomyces cerevisiae]
26891	26891	26	AA128719	Hs 22282	ESTs
7690	26891	26	AA292659	Hs 93967	ESTs
11308	26891	26	AA215299	Hs 70930	Homo sapiens chromosome 19 contig R30723
4086	26891	26	AA207114	Hs 27842	ESTs
39615	26891	26	U24704	Hs 111709	Human embryonic factor-1 mRNA complete cds
11919	26891	26	AA396938	EST - RC_AA598938	
37433	26891	26	AA258189	Hs 32471	ESTs
5587	26891	26	AA454103	Hs 110031	ESTs
18841	26891	26	X13482	Hs 81506	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'
10655	26891	26	H59617	Hs 5199	ESTs highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Drosophila melanogaster]
31574	26891	26	AA060882	Hs 10290	ESTs
7614	26891	26	N71303	Hs 50015	EST
7090	26891	26	AA009513	Hs 102696	ESTs highly similar to Ye007c-ep [S. cerevisiae]
24219	26891	26	W65960	Hs 103300	Homo sapiens epithelium fibroblast protein 2 (DPH2) mRNA complete cds
19070	26891	26	H05970	Hs 19418	ESTs
17719	26891	26	AA136569	Hs 133028	Human clone Z0900 mRNA sequence
8613	26891	26	AA227251	Hs 144295	EST
13066	26891	26	AA459555	Hs 20972	ESTs
39522	26891	26	AA478319	Hs 31821	Homo sapiens mRNA for KIAA0848 protein partial cds
1795	26891	26	F03605	Hs 5237	ESTs
14746	26891	26	D90354	Hs 75574	PUTATIVE 60S RIBOSOMAL PROTEIN
2903	26891	26	M64920	Hs 84182	Human chromosome 3p21.1 gene sequence complete cds
12968	26891	26	AA420032	Hs 90315	Human mRNA for KIAA0007 gene partial cds
18003	26891	26	AA171592	Hs 75200	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 22) alpha isoform
42633	26891	26	V92703	Hs 7487	ESTs highly similar to PTTG gene product [R. norvegicus]
30438	26891	26	AA7204	Hs 70590	ESTs
26135	26891	26	AA743765	Hs 103239	ESTs
15437	26891	26	W27560	Hs 46680	ESTs highly similar to CSDF4.12 [C. elegans]
27748	26891	26	AA453159	Hs 78977	ESTs
32315	26891	26	R98840	Hs 41723	Human kinetase spindles protein HKSP (hKSP) mRNA complete cds
25310	26891	26	AA046745	Hs 70189	ESTs highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Hyalobacterium cutaneum]
9658	26891	26	L18991	Hs 110457	ESTs
12210	26891	26	AA293774	Hs 78006	Deoxythymidylate kinase
32826	26891	26	W07091	Hs 21261	ESTs highly similar to PROBABLE TRYPTOPHAN-L-TRNA SYNTHETASE MITOCHONDRIAL [C. elegans]
9692	26891	26	L37747	Hs 20830	Human mRNA for kinesin-related protein partial cds
27862	26891	26	AA458908	Hs 89497	LAMIN B1
17268	26891	26	AA085178	Hs 50883	ESTs
9888	26891	26	N35449	Hs 24382	ESTs
26834	26891	26	X82153	Hs 111449	ESTs highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/AP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]
5157	26891	26	U80034	Hs 82479	Mitochondrial maintenance deficient (S. cerevisiae) 3
39434	26891	26	AA497013	Hs 59346	ESTs highly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]
7500	26891	26	AA173505	Hs 65563	Human mitochondrial leucyl-tRNA synthetase precursor (MUPP) mRNA mitochondrial gene encoding mitochondrial protein complete cds
14980	26891	26	U05237	Hs 142592	ESTs
13565	26891	26	AA455999	Hs 33553	ESTs highly similar to HYPOTHETICAL 46.1 KD PROTEIN IN PHO2-POL3 INTERGENIC REGION [S. cerevisiae]
38185	26891	26	AA487508	Hs 99872	Human fetal AL-50-membrane chole 1 (FAC1) mRNA complete cds
34878	26891	26	AA284744	Hs 22151	ESTs highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]
1424	26891	26	J02645	Hs 9877	Homo sapiens mRNA for KIAA0808 protein complete cds
21878	26891	26	R32786	Hs 75510	Armadillo XI (50D) subdomain
34290	26891	26	AA236866	Hs 81613	Eukaryotic translation initiation factor 2A
16109	26891	26	AA188931	Hs 113314	ESTs
5485	26891	26	X92098	Hs 58169	Homo sapiens ribonucleosome-associated protein 1-EC mRNA complete cds
27444	26891	26	AA430160	Hs 725914	H. sapiens mRNA for transmembrane protein mp24
		25		Hs 42785	ESTs highly similar to F25H9.7 [C. elegans]

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## FIGURE 4 (CONT.)

30007	25	N27439	Hs 51652 EST1	Hs 51652 EST1	Hs 29835 EST1 Weakly similar to WD28127 [C. elegans]
27802	25	A4443702	Hs 79250 RYK receptor like tyrosine kinase	Hs 79250 RYK receptor like tyrosine kinase	Hs 103305 EST1
3390	25	S59184	A4010188	Hs 103305 EST1	Hs 90346 Homo sapiens BAC clone PG30E22 from 7q21-q31
25040	24	40417	N24006	Hs 90346	Hs 9417 EST1
18620	24	F03506	F03506	Hs 9417 EST1	Hs 87465 Human putative ATP/GTP-binding protein (HAB) mRNA complete cds
15120	24	U73524	U73524	Hs 87465	Hs 91181 Human C-1 mRNA complete cds
28813	24	D59257	D59257	Hs 91181	Hs 96097 EST1
28813	24	A4287115	A4287115	Hs 96097 EST1	Hs 8932 Homo sapiens brain expressed (ing finger protein) mRNA complete cds
34723	24	A4285277	A4285277	Hs 8932	Hs 12544 EST1
7960	24	F11087	F11087	Hs 12544 EST1	Hs 70877 EST1
18977	24	A621611	A621611	Hs 70877 EST1	Hs 24753 RAN binding protein 1
28443	24	D38076	D38076	Hs 24753	Hs 31730 Homo sapiens RRM RNA binding protein Gyr-rip (GRY-RBP) mRNA complete cds
432	24	A4233031	A4233031	Hs 31730	Hs 13055 EST1
11701	24	A4417087	A4417087	Hs 13055 EST1	Hs 95821 Human osteoblast stimulating factor mRNA complete cds
12872	24	U83717	U83717	Hs 95821	Hs 70002 EST1
4836	24	T83729	T83729	Hs 70002 EST1	Hs 108527 EST1 Weakly similar to No selection line found [C. elegans]
42700	24	A4010064	A4010064	Hs 108527 EST1	Hs 37747 EST1
28395	24	A4426291	A4426291	Hs 37747 EST1	Hs 77965 Human C1-associated RS cytoplasmic CARS-Cyp mRNA complete cds
36990	24	A4427745	A4427745	Hs 77965	Hs 9012 EST1
12916	24	A4435815	A4435815	Hs 9012 EST1	Hs 19374 EST1 Highly similar to AAC-RICH MRNA CLONE AAC3 PROTEIN [Drosophila melanogaster]
36766	24	D60063	D60063	Hs 19374 EST1	Hs 40541 EST1
14420	24	A4500322	A4500322	Hs 40541 EST1	Hs 105465 H sapiens mRNA for Sn protein F
27431	24	A4429038	A4429038	Hs 105465	Hs 3376 Homo sapiens mRNA for KIAA0704 protein partial cds
6387	24	X65372	X65372	Hs 3376	Hs 3376 Tectonemeres (DNA) II alpha (1700D)
11942	24	A4223874	A4223874	Hs 3376	Hs 23348 EST1
1407	24	J04068	J04068	Hs 23348 EST1	Hs 48555 EST1
11454	24	A4233854	A4233854	Hs 48555 EST1	Hs 31082 EST1
32278	24	W42786	W42786	Hs 31082 EST1	Hs 124275 Homo sapiens mRNA for KIAA0659 protein partial cds
21872	24	A4459254	A4459254	Hs 124275	Hs 38114 EST1 Highly similar to HYPOTHETICAL 402 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]
11828	24	A4243817	A4243817	Hs 38114	Hs 2010 Crinoidantennae
22142	24	R51382	R51382	Hs 2010	Hs 18918 EST1 Weakly similar to H3 ALU SUBFAMILY J WARNING ENTRY [H. sapiens]
13533	24	A4454807	A4454807	Hs 18918	Hs 98073 EST1
4231	24	X78121	X78121	Hs 98073 EST1	Hs 28813 EST1 Weakly similar to LINE/1 H-chain fusion protein [M. musculus]
24371	24	A4045281	A4045281	Hs 28813	Hs 30272 EST1 Moderately similar to AL5 [H. sapiens]
25766	24	A4353394	A4353394	Hs 30272	Hs 94576 EST1 Weakly similar to ORF Y0P281c [S. cerevisiae]
6163	24	A4343513	A4343513	Hs 94576	Hs 7145 EST1 Highly similar to Zinc finger protein [M. musculus]
12233	24	A4509219	A4509219	Hs 7145	Hs 15741 EST1
14371	24	A4251089	A4251089	Hs 15741	Hs 20524 EST1 Highly similar to HEXOKINASE TYPE I [Homo sapiens]
26169	24	T235399	T235399	Hs 20524	Hs 19913 EST1
23855	24	N53963	N53963	Hs 19913	Hs 20201 Homo sapiens clone 24705 mRNA sequence
20534	24	R07210	R07210	Hs 20201	Hs 20990 EST1
20837	24	A4469720	A4469720	Hs 20990	Hs 24549 EST1
21185	24	A4100925	A4100925	Hs 24549	Hs 29005 EST1
13377	24	A4278907	A4278907	Hs 29005	Hs 109437 EST1
17352	24	D51172	D51172	Hs 109437 EST1	Hs 109562 Homo sapiens mRNA for hTCT-4
11914	24	R17012	R17012	Hs 109562	Hs 120658 Human mRNA for RNA helicase complete cds
28796	24	N63354	N63354	Hs 120658	Hs 4310 EST1
22491	24	T53136	T53136	Hs 4310	Hs 46842 EST1
40847	24	A4309880	A4309880	Hs 46842	Hs 14811 Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds
42022	24	D36528	D36528	Hs 14811	
8653	24	A4281733	A4281733		
363	24	N62683	N62683		
28879	24	W42845	W42845		
31856	24				
24092	24				

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## FIGURE 4 (CONT.)

19428	22	Hs12840	EST	Hs10840	EST	Hs10840	EST	Hs10840	EST
27294	22	Aa118389	EST	Hs12219	EST	Hs12219	EST	Hs12219	EST
13500	22	Aa145288	EST	Hs12594	EST	Hs12594	EST	Hs12594	EST
13552	22	Aa145493	EST	Hs12594	EST	Hs12594	EST	Hs12594	EST
20483	22	Aa150797	EST	Hs12594	EST	Hs12594	EST	Hs12594	EST
3074	22	U02237	Human fetal ALU-53 relative clone 1 (FAC1) mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
38504	22	Z87770	EST	Hs12594	EST	Hs12594	EST	Hs12594	EST
59077	22	Aa064616	EST	Hs12594	EST	Hs12594	EST	Hs12594	EST
5948	22	A63337	EST	Hs12594	EST	Hs12594	EST	Hs12594	EST
24247	22	Hs108781	Ribosome protein L37	Hs12594	EST	Hs12594	EST	Hs12594	EST
40879	22	Hs108781	Ribosome protein L37	Hs12594	EST	Hs12594	EST	Hs12594	EST
5075	22	Hs108781	Ribosome protein L37	Hs12594	EST	Hs12594	EST	Hs12594	EST
9239	22	D719100	Membrane cofactor protein (CD44) lymphocyte cross-reactive antigen	Hs12594	EST	Hs12594	EST	Hs12594	EST
41987	22	Hs109528	EST	Hs12594	EST	Hs12594	EST	Hs12594	EST
35655	22	F04320	Repetitive factor C37-40 subunit	Hs12594	EST	Hs12594	EST	Hs12594	EST
7404	22	Aa049498	Hs17351 Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
8388	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
14329	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
21197	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
22603	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
39120	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
4074	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
26756	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
11587	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
23550	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
41933	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
26955	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
3343	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
42435	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
5907	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
25756	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
34164	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
8072	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
7387	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
18016	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
20843	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
10054	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
34094	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
41246	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
22934	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
19666	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
28446	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
651	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
20221	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
5792	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
29656	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
19240	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
11668	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
14152	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
38341	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
11800	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
39085	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
4046	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
11600	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
5051	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST
20674	22	Hs17351	Homo sapiens voltage dependent anion channel protein mRNA complete cds	Hs12594	EST	Hs12594	EST	Hs12594	EST

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## FIGURE 4 (CONT.)

41031	2.2	H91246	Hs.102897	ESTs	Hs.102897	ESTs	
24711	2.2	Z39045	Hs.21470	ESTs	Hs.21470	ESTs	
4733	2.2	U96558	Hs.57089	Human uni-down protein mRNA within the p53 exon 1 complete cds	Hs.57089	Human uni-down protein mRNA within the p53 exon 1 complete cds	
29733	2.2	H93398	Hs.42880	EST	Hs.42880	EST	
23135	2.2	130359	Hs.28815	ESTs	Hs.28815	ESTs	
34638	2.2	AA297827	Hs.104473	EST	Hs.104473	EST	
1889	2.2	C20391	Hs.13378	Arpican III (p6ocarin III)	Hs.13378	Arpican III (p6ocarin III)	
4136	2.2	U26014	Hs.74122	ICH-2 PROTEASE PRECURSOR	Hs.74122	ICH-2 PROTEASE PRECURSOR	
20276	2.2	N32919	Hs.27931	ESTs	Hs.27931	ESTs	
18258	2.2	AA203380	Hs.41145	ESTs	Hs.41145	ESTs	
13250	2.1	AA446459	Hs.27399	ESTs	Hs.27399	ESTs	
34370	2.1	AA251029	Hs.104058	ESTs Weakly similar to HYPOTHETICAL 27.4 KO PROTEIN IN MER2.CP87 INTERGENIC REGION [Saccharomyces cerevisiae]	Hs.104058	ESTs Weakly similar to HYPOTHETICAL 27.4 KO PROTEIN IN MER2.CP87 INTERGENIC REGION [Saccharomyces cerevisiae]	
27896	2.1	AA470156	Hs.80449	ESTs Weakly similar to Open 74K chain cytosolic [Rhoneglous]	Hs.80449	ESTs Weakly similar to Open 74K chain cytosolic [Rhoneglous]	
10804	2.1	AA095549	Hs.18479	ESTs	Hs.18479	ESTs	
34552	2.1	AA271985	Hs.10389	Human mRNA for KIAA0272 gene complete cds	Hs.10389	Human mRNA for KIAA0272 gene complete cds	
16380	2.1	AA271119	Hs.70256	ESTs	Hs.70256	ESTs	
37415	2.1	AA453907	Hs.99349	EST	Hs.99349	EST	
14582	2.1	AA4821340	Hs.10060	ESTs Weakly similar to HYPOTHETICAL 39.8 KO PROTEIN IN MTD1.HUP133 INTERGENIC REGION [Saccharomyces cerevisiae]	Hs.10060	ESTs Weakly similar to HYPOTHETICAL 39.8 KO PROTEIN IN MTD1.HUP133 INTERGENIC REGION [Saccharomyces cerevisiae]	
5173	2.1	U81354	Hs.51171	Human sapiens signal recognition particle 72 (SRP72) mRNA complete cds	Hs.51171	Human sapiens signal recognition particle 72 (SRP72) mRNA complete cds	
18972	2.1	H93639	Hs.33778	ESTs	Hs.33778	ESTs	
23301	2.1	T31847	Hs.13004	ESTs	Hs.13004	ESTs	
20504	2.1	N52066	Hs.142838	ESTs	Hs.142838	ESTs	
40145	2.1	H81391	Hs.81187	Human mRNA for histamine N-methyltransferase complete cds	Hs.81187	Human mRNA for histamine N-methyltransferase complete cds	
3461	2.1	S75256	Hs.51251	ESTs	Hs.51251	ESTs	
38021	2.1	AA418876	Hs.5169	ESTs Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521 [H. sapiens]	Hs.5169	ESTs Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521 [H. sapiens]	
5807	2.1	X55740	Hs.76656	5' nucleotidase (CDV3)	Hs.76656	5' nucleotidase (CDV3)	
38155	2.1	AA488777	Hs.105698	ESTs	Hs.105698	ESTs	
624	2.1	HG1112-411112	EST - HG1112-411112				
8384	2.1	AA424282	Hs.91728	Human T5-4D subunit (PIL-Sc1) mRNA complete cds	Hs.91728	Human T5-4D subunit (PIL-Sc1) mRNA complete cds	
25165	2.1	AA027837	Hs.30703	Reclins pigmentosa 3 (C-3) (dried recessive)	Hs.30703	Reclins pigmentosa 3 (C-3) (dried recessive)	
24348	2.1	W88489	Hs.77899	Tropomyosin alpha chain (striated muscle)	Hs.77899	Tropomyosin alpha chain (striated muscle)	
35340	2.1	AA398900	EST - RC_AA398900				
10898	2.1	AA112063	Hs.15313	ESTs Weakly similar to PRE mRNA SPLICING HELICASE BIR2 [S. cerevisiae]	Hs.15313	ESTs Weakly similar to PRE mRNA SPLICING HELICASE BIR2 [S. cerevisiae]	
381	2.1	D28473	Hs.78770	Isoluciferase-RNA synthetase	Hs.78770	Isoluciferase-RNA synthetase	
22051	2.1	R49047	Hs.31875	ESTs Weakly similar to [H. ALU SUBFAMILY J] WARNING ENTRY III [H. sapiens]	Hs.31875	ESTs Weakly similar to [H. ALU SUBFAMILY J] WARNING ENTRY III [H. sapiens]	
11528	2.1	AA230018	Hs.10724	ESTs Weakly similar to unknown [S. cerevisiae]	Hs.10724	ESTs Weakly similar to unknown [S. cerevisiae]	
11890	2.1	AA278323	Hs.17481	Human sapiens clone 24008 mRNA sequence	Hs.17481	Human sapiens clone 24008 mRNA sequence	
5448	2.1	X02751	Hs.69855	Neuroblastoma RAS viral (N-ras) oncogene homolog	Hs.69855	Neuroblastoma RAS viral (N-ras) oncogene homolog	
35956	2.1	AA412533	Hs.105571	ESTs	Hs.105571	ESTs	
7525	2.1	AA169259	Hs.88851	ESTs	Hs.88851	ESTs	
39592	2.1	F09351	Hs.16492	ESTs Weakly similar to S. cerevisiae PTM1 precursor [C. elegans]	Hs.16492	ESTs Weakly similar to S. cerevisiae PTM1 precursor [C. elegans]	
28020	2.1	AA478479	Hs.71992	ESTs	Hs.71992	ESTs	
18425	2.1	AA232103	Hs.59112	ESTs	Hs.59112	ESTs	
33368	2.1	W60814	Hs.47283	ESTs	Hs.47283	ESTs	
20590	2.1	N58146	Hs.34227	ESTs	Hs.34227	ESTs	
12907	2.1	AA427577	Hs.26502	ESTs	Hs.26502	ESTs	
22858	2.1	T10264	Hs.116122	ESTs	Hs.116122	ESTs	
38	2.1	AB003096	Hs.28653	Human sapiens mRNA for Coc7-related kinase complete cds	Hs.28653	Human sapiens mRNA for Coc7-related kinase complete cds	
14350	2.1	AA586831	Hs.17121	ESTs	Hs.17121	ESTs	
25593	2.1	AA113149	Hs.8130	Human sapiens IPL (PL) mRNA complete cds	Hs.8130	Human sapiens IPL (PL) mRNA complete cds	
26529	2.1	AA278594	Hs.68461	EST	Hs.68461	EST	
6681	2.1	Y00911	Hs.2910	Phosphotransferase kinase 2	Hs.2910	Phosphotransferase kinase 2	
18878	2.1	AA056538	Hs.63314	ESTs	Hs.63314	ESTs	
38040	2.1	AA481403	Hs.107213	ESTs	Hs.107213	ESTs	
4111	2.1	U26312	Hs.83550	Human histone H4 protein HP1H4-gamma mRNA complete cds	Hs.83550	Human histone H4 protein HP1H4-gamma mRNA complete cds	

**FIGURE 4 (CONT.)**

31	W07449	Hs A1234	ESTs	
31	A024935	Hs B5032	ESTs	
31	Z5311	Hs 12358	Human saproin GDP-L-Luciferin synthetase (GFP) mRNA, complete cds	
31	Z60010	Hs 105351	ESTs	
31	A441148	Hs 85379	Cytochrome c oxidase subunit I/b	
31	AC009115	Hs 81343	Cytochrome c oxidase subunit I/b	
31	Z71681	Hs 31748	For TRE5	
31	A466075	Hs 48795	Human saproin mRNA for plasine RNA helicase 3' end	
31	A058505	Hs 112180	Zinc finger protein 148 (P42-52)	
31	U08951	Hs B9860	Cytochrome oxidase (cytochrome c oxidase)	
31	O16611	EST - A4147425_5		
31	A1171425	Hs 124852	ESTs	
31	14701	DS9324	EST - C79423	
31	300	D28423	Hs 79375	Hydroxycinnamoyl lythylase (beta-hydroxycinnamoyl-Coenzyme A-carboxylase (ATP-hydroxycinnamyl) ligase)
31	325	D07378	Hs 2131	Arginine vasopressin receptor 1 (AVPR1)
31	8957	U19006	EST - C28364	
31	377	D28364	Hs 42582	ESTs
31	208719	A0609710	Hs 42582	ESTs
31	7322	A00006932	Hs 135552	ESTs
31	203158	U19041	ESTs	RC_W1106411
31	24230	W77278	Hs 5550	ESTs
31	140712	H46553	Hs 9504	Human clone 121711 derivative, manner transcription internal mRNA sequence
31	36319	A4415107	Hs 97010	ESTs
31	256514	A4176951	Hs 110957	ESTs
31	16344	A0148007	Hs 5427	ESTs
31	8116	A3788993	Hs 104559	ESTs
31	79962	N22228	Hs 27348	ESTs
31	32206	R49327	Hs 57435	Natural resistance-associated macrophage protein 2
31	37972	A4479215	EST - RC_A4479215	
31	34364	A4292555	Hs 06557	ESTs

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FIGURE 5

Primary Key	fold downregulated of Tumor vs	Accession	Unigene CLUSTER	Unigene Descriptor
2348	>10	M15656	Hs.75592	Aldolase B fructose-bisphosphate
6463	>10	X90908	Hs.74126	H.sapiens mRNA for I-15P (I-BABP) protein
42139	>10	T73335	Hs.93194	AFOLIPOPROTEIN A-1 PRECURSOR
4544	>10	U48959	Hs.75950	H.sapiens mRNA for myosin light chain kinase
1583	>10	K02765	Hs.58512	COMPLEMENT C3 PRECURSOR
2426	>10	M19828	Hs.585	Apolipoprotein B (including Ag(x) antigen)
8859	>10	AB002351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z38688	Hs.24192	ESTs
17610	>10	AA151402	Hs.46531	ESTs
7006	>10	Z70295	Hs.32966	H.sapiens mRNA for GCAP-II/uroguanylin precursor
1304	>10	HG4310-	Hs.65424	EST - HG4310-HT4580
5980	>10	X64559	Hs.121713	Tetranectin (plasminogen-binding protein)
41987	>10	T47089	Hs.3807	Cytochrome P450 subfamily XXI (steroid 21-hydroxylase congenital adrenal hyperplasia)
24461	>10	W94427	Hs.89552	ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus
2372	>10	M16594	Hs.89552	Glutathione S-transferase A2
6001	>10	X65727	Hs.89552	Glutathione S-transferase A2
1750	>10	L10955	Hs.89485	Carbonic anhydrase IV
15130	>10	U77643	Hs.95655	Homo sapiens K12 protein precursor mRNA complete cds
12467	>10	AA402656	Hs.28284	ESTs
41148	>10	R06984	Hs.50404	EST - RC_R06984_s
31652	>10	N73958	Hs.50404	Human chemokine (TECK) mRNA complete cds
4605	>10	U51010	EST - U51010	EST - U51010
28359	>10	AA609133	Hs.58115	ESTs
24066	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194	Hs.80552	ESTs
12084	>10	AA284767	Hs.21910	ESTs
41473	>10	R48732	Hs.11006	ESTs
27108	>10	AA404397	Hs.58414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
2848	>10	M56286	Hs.159	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR
19537	>10	H30270	Hs.32583	ESTs
18784	>10	F09748	Hs.7974	ESTs
5773	>10	X54162	Hs.79386	64 KD AUTOANTIGEN D1



## FIGURE 5 (CONT.)

27387	>10	AA426330	Hs.78264	ESTs
2866	>10	M59815	Hs.76682	Complement component 4A
42530	>10	W72859	Hs.74669	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]
827	>10	D87433	Hs.84753	Human mRNA for KIAA0246 gene partial cds
650	>10	D78014	Hs.74566	Human mRNA for dihydropyrimidinase related protein-3 complete cds
7026	>10	Z80345	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
16736	>10	AA045306	Hs.42996	ESTs
4630	>10	U52101	Hs.9999	Human YMP mRNA complete cds
4655	>10	U52969	Hs.80296	BRAIN SPECIFIC POLYPEPTIDE PEP-19
42758	>10	Z41411	Hs.107040	ESTs
35537	>10	AA402933	Hs.29283	ESTs
40392	>10	H99587	Hs.108880	ESTs
7354	>10	AA092348	Hs.7858	ESTs
9034	>10	C01833	Hs.29759	ESTs Weakly similar to III ALU SUBFAMILY SX WARNING ENTRY III [H.sapiens]
10935	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]
5520	>10	X06256	Hs.119218	Integrin alpha 5 (fibronectin receptor alpha polypeptide)
2547	>10	M25809	Hs.1009	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 56/58kD isoform 1
9003	>10	C00808	Hs.107882	ESTs
41628	>10	R70212	Hs.79630	Immunoglobulin-associated alpha
21934	>10	R44449	Hs.48778	ESTs
11129	8	AA156873	Hs.15970	ESTs
40387	7	H99460	Hs.108873	ESTs

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FIGURE 6

Primary Key	fold downregulated of Tumor	Accession	Unigene CLUSTER	Unigene Descriptor
2348	>10	M15656	Hs.75592	Aldolase B fructose-bisphosphate
6463	>10	X90908	Hs.74126	H.sapiens mRNA for l-15P (l-BABP) protein
42139	>10	T73335	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
4544	>10	U48959	Hs.75950	H.sapiens mRNA for myosin light chain kinase
1583	>10	K02765	Hs.58512	COMPLEMENT C3 PRECURSOR
2426	>10	M19828	Hs.585	Apolipoprotein B (including Ag(X) antigen)
8859	>10	AB002351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z38688	Hs.24192	ESTs
17810	>10	AA151402	Hs.46531	ESTs
7006	>10	Z70295	Hs.32966	H.sapiens mRNA for GCAP-4/uroguanylin precursor
1304	>10	HG4310	EST - HG4310-HT4580	
5980	>10	X64559	Hs.65424	Tetranectin (plasminogen-binding protein)
41987	>10	T47089	Hs.121713	Cytochrome P450 subfamily XXI (steroid 21-hydroxylase congenital adrenal hyperplasia)
24461	>10	W94427	Hs.3807	ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus musculus]
2372	>10	M16594	Hs.89552	Glutathione S-transferase A2
6001	>10	X65727	Hs.89552	Glutathione S-transferase A2
1750	>10	L10955	Hs.89485	Carbonic anhydrase IV
15130	>10	U77643	Hs.95655	Homo sapiens K12 protein precursor mRNA complete cds
12467	>10	AA402656	Hs.28264	ESTs
41148	>10	R06984	EST - RC_R06984_s	
31652	>10	N73958	Hs.50404	Human chemokine (TECK) mRNA complete cds
23483	>10	T88873	Hs.143289	H.sapiens mRNA for metallothionein isoform 1R
4605	>10	U51010	EST - U51010	
28359	>10	AA609133	Hs.58115	ESTs
24066	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194	Hs.80552	ESTs
12084	>10	AA284767	Hs.21910	ESTs
41473	>10	R48732	Hs.11006	ESTs
32568	>10	T29248	Hs.143113	Human pancreatic lipase related protein 2 (PLRP2) mRNA complete cds
6413	>10	X87159	Hs.37129	Sodium channel nonvoltage-gated 1 beta (Liddle syndrome)
20707	>10	N64436	Hs.20813	ESTs
27108	>10	AA404397	Hs.58414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
12477	>10	AA403032	Hs.21701	ESTs
42059	>10	T61654	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
25468	>10	AA079072	Hs.1477	Insulin-like growth factor binding protein 6
26910	>10	AA303081	Hs.78293	ESTs

FIGURE 6 (CONT.)

16938	>10	AA059473	Hs.56783	ESTs	
41788	>10	T03735	Hs.26885	ESTs	
7754	>10	AA234634	Hs.76722	Human NF-IL6-beta protein mRNA complete cds	
6122	>10	X72012	Hs.75962	Endoglin (Oster-Rendu-Weber syndrome 1)	
2848	>10	M58286	Hs.159	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR	
23013	>10	T18661	Hs.6725	ESTs	
19537	>10	H30270	Hs.32583	ESTs	
4584	>10	U50360		EST - U50360	
37410	>10	AA453652	Hs.39344	ESTs	
27969	>10	AA464594	Hs.63382	ESTs	
35497	>10	AA400606	Hs.144344	EST	
37013	>10	AA443690	Hs.136268	ESTs Highly similar to ZINC FINGER PROTEIN HF 12 [Homo sapiens]	
39247	>10	AA621553	Hs.112998	ESTs	
13471	>10	AA452598	Hs.109590	ESTs	
42110	>10	T68878	Hs.76688	Carboxylesterase 2 (liver)	
10965	>10	AA128997	Hs.18953	Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA complete cds	
4918	>10	U67733	Hs.3831	Human cGMP-stimulated 3',5'-cyclic nucleotide phosphodiesterase PDE2A3 (PDE2A) mRNA complete cds	
40737	>10	N54950	Hs.81454	H.sapiens KHK mRNA for kalchexokinase clone pHKH3a	
30403	>10	N45300	Hs.110647	Meis1 (mouse) homolog	
11432	>10	AA233369	Hs.361	ESTs	
18784	>10	F09748	Hs.7974	ESTs	
40662	>10	N49281		EST - RC_N49281	
5773	>10	X54162	Hs.79386	64 KD AUTOANTIGEN D1	
35041	>10	AA350586	Hs.30862	ESTs	
20668	>10	N70068	Hs.7243	ESTs	
39729	>10	H11489	Hs.105805	ESTs	
27387	>10	AA426330	Hs.78264	ESTs	
39758	>10	H15814	Hs.80485	Human apM1 mRNA for GS3109 (novel adipose specific collagen-like factor) complete cds	
4319	>10	U37283	Hs.58882	Human microfibril-associated glycoprotein-2 MAGP-2 mRNA complete cds	
2866	>10	M59815	Hs.76682	Complement component 4A	
30332	>10	N39075	Hs.44934	EST	
41344	>10	R40189	Hs.6985	ESTs	
28271	>10	AA521200	Hs.48778	ESTs	
5834	>10	X57129	Hs.7644	HISTONE H1D	
19048	>10	H05464	Hs.100251	ESTs	
1429	>10	J02854	Hs.9615	Human 20-kDa myosin light chain (MLC-2) mRNA complete cds	
19491	>10	H27910	Hs.107384	ESTs	
29992	>10	N26386	Hs.33084	Solute carrier family 2 (facilitated glucose transporter) member 5	
2041	>10	L36033	Hs.77423	Stromal cell-derived factor 1	
22665	>10	R99909	Hs.36186	ESTs	

## FIGURE 6 (CONT.)

11624	>10	AA243654	Hs.17998	ESTs	
12512	>10	AA405189	Hs.20733	ESTs	
41443	>10	R45577	Hs.10683	ESTs	
5055	>10	U77180	Hs.50002	Human mRNA for EB1-ligand chemokine complete cds	
6038	>10	X66945	Hs.748	Basic fibroblast growth factor (bFGF) receptor (shorter form)	
42530	>10	W72859	Hs.74669	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]	
827	>10	D87433	Hs.94753	Human mRNA for KIAA0246 gene partial cds	
650	>10	D78014	Hs.74566	Human mRNA for dihydropyrimidinase related protein-3 complete cds	
37350	>10	AA452606	Hs.99289	EST	
37488	>10	AA455178	Hs.99397	ESTs	
36646	>10	AA431797	Hs.98763	EST	
38999	>10	AA609907	EST - RC_AA609807		
38191	>10	AA487895	Hs.17311	ESTs	
9944	>10	N57484	Hs.74670	Human mRNA for KIAA0146 gene partial cds	
8139	>10	AA341723	Hs.107374	ESTs	
41522	>10	RS3966	Hs.75092	N-CHIMAERIN	
38090	>10	AA482603	Hs.111301	Matrix metalloproteinase 2 (gelatinase A 72kD gelatinase 72kD type IV collagenase)	
41175	>10	R09241	EST - RC_R09241		
36947	>10	AA437388	Hs.115726	ESTs	
4175	>10	U29953	Hs.76110	Pigment epithelium-derived factor	
35421	>10	AA399686	Hs.97669	EST	
4358	>10	U39487	Hs.250	Xanthine dehydrogenase	
35463	>10	AA400272	Hs.97758	EST	
7026	>10	Z80345	Hs.127610	Acy-Coenzyme A dehydrogenase C-2 to C-3 short chain	
34625	>10	AA282238	Hs.118463	Homo sapiens clone 24519 unknown mRNA partial cds	
20179	>10	N24879	Hs.9693	ESTs	
36805	>10	AA435901	Hs.56874	ESTs Weakly similar to p20 protein [R.norvegicus]	
24447	>10	W93121	Hs.23841	Human mRNA for KIAA0355 gene complete cds	
10247	>10	R74386	Hs.108924	ESTs	
3618	>10	U02388	Hs.101	Leukotriene B4 omega hydroxylase (cytochrome P450 subfamily IVF)	
1464	>10	J03474	Hs.3157	SERUM AMYLOID A PROTEIN PRECURSOR	
16842	>10	AA055163	Hs.57975	Homo sapiens mRNA for cardiac calsequestrin complete cds	
16736	>10	AA045306	Hs.42996	ESTs	
22666	>10	R85880	Hs.33455	ESTs	
5248	>10	U86358	Hs.50404	Human chemokine (TECK) mRNA complete cds	
7510	>10	AA136353	Hs.38022	ESTs	
34683	>10	AA284920	Hs.13716	ESTs	
19986	>10	H89980	Hs.12112	ESTs Moderately similar to protein phosphatase 1 binding protein PTG [M.musculus]	
9959	>10	N75215	Hs.43148	ESTs	
38136	>10	AA486185	Hs.125176	ESTs	

## FIGURE 6 (CONT.)

36702	>10	AA434108	Hs.101393	ESTs Moderately similar to DNAJ PROTEIN HOMOLOG 1 [Homo sapiens]
3357	>10	M99487	Hs.1915	PROSTATE-SPECIFIC MEMBRANE ANTIGEN
36783	>10	AA435805	Hs.112065	EST
4876	>10	U68051	Hs.2048	Protease serine 2 (trypsin 2)
41149	>10	R06986	Hs.76487	ESTs
15925	>10	Y13492	Hs.78483	Homo sapiens mRNA for smoothelin
12944	>10	AA428258	Hs.8769	ESTs
9317	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
19331	>10	H17865	Hs.23213	ESTs
5032	>10	U74382	Hs.90357	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds
34299	>10	AA235009	Hs.32246	ESTs
32852	>10	W31906	Hs.116428	ESTs
6432	>10	X89066	Hs.94413	Transient receptor potential channel 1
37001	>10	AA443311	Hs.98998	ESTs
4630	>10	U52101	Hs.9999	Human YMP mRNA complete cds
19489	>10	H27852	Hs.28137	ESTs
23028	>10	T17215	Hs.6952	ESTs
33359	>10	AA398061	Hs.112561	ESTs Moderately similar to PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR [H.sapiens]
4655	>10	U52969	Hs.80296	BRAIN SPECIFIC POLYPEPTIDE PEP-19
26030	>10	AA235984	Hs.87469	ESTs
41348	>10	R40395	Hs.112125	Lecithin-cholesterol acyltransferase
14494	>10	AA609645	Hs.25632	ESTs Weakly similar to PNG gene [H.sapiens]
4453	>10	U43916	Hs.79368	Human epithelial membrane protein (CL-20) mRNA complete cds
42758	>10	Z41411	Hs.107040	ESTs
35637	>10	AA402933	Hs.29283	ESTs
40392	>10	H99587	Hs.108880	ESTs
19366	>10	H19204	Hs.133466	ESTs
5184	>10	U82169	Hs.87234	Human f1322 homolog (FZD3) mRNA complete cds
859	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
1595	>10	K03207	Hs.103972	Salivary proline-rich protein
15574	>10	W38778	Hs.26216	ESTs
8985	>10	C00125	Hs.24332	ESTs Weakly similar to deoxyribose-phosphate aldolase [C.elegans]
33955	>10	AA182845	Hs.139088	Homo sapiens FIP2 alternatively translated mRNA complete cds
7949	>10	AA283620	Hs.34956	ESTs
11670	>10	AA252191	Hs.25199	Homo sapiens PAC clone DJ130H16 from 22q12.1-qter
7354	>10	AA092348	Hs.7858	ESTs
36151	>10	AA419011	Hs.96744	ESTs
42136	>10	T72491	Hs.73849	Apolipoprotein C-III
289	>10	D16480	Hs.75860	Hydroxyacyl-Coenzyme A dehydrogenase3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein) alpha subunit
41379	>10	R42233	Hs.106487	Homo sapiens mRNA for KIAA0673 protein partial cds

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FIGURE 6 (CONT.)

34764	>10	AA287870	Hs.890	Lympholysin-beta
24515	>10	Z38289	Hs.12701	ESTs
18652	>10	F03111	Hs.22505	ESTs
37815	>10	AA469952	Hs.97899	ESTs
9034	>10	C01833	Hs.29759	ESTs Weakly similar to IIII ALU SUBFAMILY SX WARNING ENTRY IIII [H.sapiens]
34805	>10	AA291522	Hs.97250	EST
12246	>10	AA348198	Hs.14829	Homo sapiens mRNA for GABA-BR1a (nGB1a) receptor
42153	>10	T77729	Hs.89890	Pyruvate carboxylase
27110	>10	AA404494	Hs.84112	CTP synthetase
28831	>10	D59722	Hs.92924	ESTs
6333	>10	X82494	Hs.2853	Fibulin 2
10935	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]
27257	>10	AA418001	Hs.46146	ESTs Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]
3631	>10	U03090	Hs.290	Homo sapiens Cdz-dependent phospholipase A2 mRNA complete cds
4752	>10	U59632	Hs.3847	Glycoprotein Ib (platelet) beta polypeptide
3766	>10	U09579	Hs.74984	CYCLIN-DEPENDENT KINASE INHIBITOR 1
4310	>10	U37055	Hs.76034	Macrophage stimulating 1 (hepatocyte growth factor-like)
26923	>10	AA342302	Hs.55036	ESTs
5520	>10	X06256	Hs.119218	Integrin alpha 5 (fibronectin receptor alpha polypeptide)
16720	>10	AA044732	Hs.77208	ESTs
25336	>10	AA053405	Hs.101404	ESTs
2547	>10	M25809	Hs.1009	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 56/58kD isoform 1
9796	>10	M63509	Hs.73974	Glutathione S-transferase M2 (muscle)
5206	>10	U82979	Hs.67846	Human clone HM18 monocyte inhibitory receptor precursor mRNA complete cds
9377	>10	H12674	Hs.9396	ESTs
41960	>10	T33511	Hs.4844	ESTs
21911	>10	R43980	Hs.26320	ESTs
16225	>10	AA011305	Hs.10029	Calthepsin C
16071	>10	AA001426	Hs.40863	ESTs
29335	>10	H68239	Hs.39122	ESTs
34866	>10	AA344866	Hs.1285	Complement component 8 gamma polypeptide
21076	>10	N99976	Hs.8016	ESTs
4402	>10	U41518	Hs.74502	AQUAPORIN-CHIP
20423	>10	N49308	Hs.104938	ESTs
16575	>10	AA031948	Hs.57548	ESTs
28264	>10	AA521080	Hs.46765	ESTs
9003	>10	C00808	Hs.107882	ESTs
5632	>10	X15357	EST - X15357	
20852	>10	N69540	Hs.17713	ESTs
34585	>10	AA281002	Hs.40735	ESTs

## FIGURE 6 (CONT.)

33690	>10	Z38607	Hs.62248	ESTs	
8904	>10	AF002256	Hs.86180	Homo sapiens killer cell receptor (KIR103) mRNA allele ASD1 complete cds	
3307	>10	M95809	Hs.89578	BASIC TRANSCRIPTION FACTOR 62 KO SUBUNIT	
39200	>10	AA621246	Hs.112956	EST	
24712	>10	Z39652	Hs.27457	ESTs	
2199	>10	L49169	Hs.75678	Human GOS3 mRNA complete cds	
39942	>10	AA609646	Hs.94970	Human mRNA for KIAA0306 gene partial cds	
41628	>10	R70212	Hs.79630	Immunoglobulin-associated alpha	
6834	>10	Z18954	Hs.29650	S100 calcium-binding protein A5 (formerly S100D)	
40562	>10	N33212	Hs.107197	ESTs	
37333	>10	AA452158	Hs.75122	TRANSFORMING PROTEIN RHOB	
3992	>10	U19713	Hs.76364	Allograft inflammatory factor 1	
38734	>10	AA608792	Hs.112591	EST	
37836	>10	AA470135	Hs.112238	ESTs	
10000	>10	N79674	Hs.7915	ESTs	
30658	>10	N51105	Hs.111223	ESTs	
17629	>10	AA131919	Hs.69009	ESTs	
36260	>10	AA423970	Hs.98378	ESTs	
24122	>10	W46947	Hs.4188	ESTs	
1066	>10	HG2705-	EST - HG2705-HT2801		
12389	>10	AA399633	Hs.24872	ESTs	
26025	>10	AA235874	Hs.88868	PUTATIVE DNA BINDING PROTEIN A20	
41104	>10	R01398	EST - RC_R01398		
33586	>10	W93015	Hs.73166	Treacher Collins syndrome susceptibility protein	
25379	>10	AA058893	Hs.111841	Human adenoviral cyclase-associated protein homolog CAP2 (CAP2) mRNA complete cds	
17907	>10	AA160530	Hs.72447	ESTs	
36838	>10	AA436163	Hs.95851	Homo sapiens Plg12 (Plg12) mRNA complete cds	
19524	>10	H29586	Hs.83468	Homo sapiens clone 23579 mRNA sequence	
21934	>10	R44449	Hs.48778	ESTs	
32456	>10	T15829	Hs.65264	ESTs	
15440	>10	W27301	Hs.111652	ESTs Moderately similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA [Thermomonospora curvata]	
2807	>10	M55210	Hs.87428	Laminin gamma 1 (formerly LAMB2)	
34193	>10	AA232251	Hs.128630	ESTs	
14584	>10	AA621414	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds	
38752	>10	AA608852	Hs.112803	EST	
5294	>10	U90065	Hs.79351	Human two P-domain K+ channel TWIK-1 mRNA complete cds	
84	>10	AF001359	EST - AF001359_f		
4856	>10	U65093	Hs.82071	Human msg1-related gene 1 (mrg1) mRNA complete cds	
13974	>10	AA479299	Hs.21107	ESTs	
26151	>10	AA250836	Hs.108509	ESTs	

## FIGURE 6 (CONT.)

5938	>10	X62535	Hs.74044	Diacylglycerol kinase alpha (80kD)
17717	>10	AA136541	Hs.71647	EST
12404	>10	AA400292	Hs.23786	ESTs
2407	>10	M18737	Hs.90708	GRANZYME A PRECURSOR
26620	10	AA280413	Hs.89843	Spleen focus forming virus (SFFV) proviral integration oncogene spl1
37675	10	AA460377	Hs.99816	ESTs
41827	10	T15445	Hs.99491	H.sapiens mRNA for F2583.3 kinase like protein from C.elegans
82	10	AF000959	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
203	10	D12620	Hs.106242	CYTROCHROME P450 IVF3
24159	10	W57862	Hs.21289	ESTs
5302	10	U90543	Hs.79041	Human butyrophilin (BTF1) mRNA complete cds
2219	10	L76670	Hs.109610	Homo sapiens nkat7 mRNA complete cds
24392	10	W88568	Hs.58589	Homo sapiens glycogenin-2 gamma (glycogenin-2) mRNA complete cds
36159	10	AA419279	Hs.82813	Colony-stimulating factor 1 (M-CSF)
28251	10	AA504512	Hs.76852	ESTs Weakly similar to ZK792.1 [C.elegans]
37592	10	AA458668	Hs.95898	ESTs
39619	9	F10640	Hs.12354	ESTs
8240	9	AA397841	Hs.106879	ESTs
10887	9	AA101632	Hs.22971	ESTs
37500	9	AA455474	Hs.100530	ESTs
42650	9	W92272	Hs.25601	Homo sapiens zinc-finger helixcase (hZFh) mRNA complete cds
9011	9	C01394	Hs.106823	Homo sapiens clone 24818 mRNA sequence
3490	9	S77763	Hs.75643	Homo sapiens NF-E2 protein (NF-E2) mRNA complete cds
36691	9	AA432381	Hs.97357	ESTs Moderately similar to NITRIC OXIDE SYNTHASE INDUCIBLE [H.sapiens]
3478	9	S76992	Hs.104005	Vav 2 oncogene
42034	9	T56281	Hs.110440	Human metallothionein (MT1)-F gene
11845	9	AA259064	Hs.10839	ESTs Weakly similar to unknown [S.cerevisiae]
19317	9	H17476	Hs.11615	ESTs Weakly similar to dual specificity phosphatase [H.sapiens]
42395	8	W42733	Hs.109870	ESTs
11425	8	AA233257	Hs.25511	Homo sapiens mRNA for Hic-5 partial cds
15310	8	W19098	Hs.7921	ESTs
36601	8	AA431337	Hs.98017	ESTs
13499	8	AA453458	Hs.7301	ESTs
37514	8	AA455914	Hs.1019	Parathyroid hormone receptor 1
5988	8	X65644	Hs.75063	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2
33589	8	W93074	Hs.59342	ESTs
5801	8	X55448	Hs.3118	H.sapiens mRNA for 2.19 gene
11129	8	AA156873	Hs.15970	ESTs
31987	8	N94551	Hs.55060	ESTs
40438	8	NZ1684	Hs.80500	Human mRNA for KIAA0061 gene partial cds



## FIGURE 6 (CONT.)

34471	8	AA258843	Hs.111376	ESTs	
25530	8	AA098834	Hs.83428	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	
39471	7	O60265	Hs.107894	ESTs	
25100	7	AA019426	Hs.103343	EST	
15915	7	Y09858	Hs.82577	Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34) hypothetical protein E	
19097	7	H08171	Hs.30842	ESTs	
35353	7	AA398962	Hs.97699	ESTs	
36822	7	AA435978	Hs.98852	EST	
35530	7	AA400893	Hs.41717	Human 3'5' cyclic nucleotide phosphodiesterase (HSPDE1A3A) mRNA complete cds	
3869	7	U14417	Hs.106185	Human Rat guanine nucleotide dissociation stimulator mRNA partial cds	
1978	7	L29339	Hs.1964	Solute carrier family 5 (sodium/glucose cotransporter) member 1	
26178	7	AA251153	Hs.27910	Homo sapiens centromeric Nek2-associated protein 1 (C-NAP1) mRNA complete cds	
36428	7	AA427605	Hs.98551	Human cardiac myosin binding protein-C (MyBP-C) gene complete cds	
26333	7	AA256075	Hs.82280	Homo sapiens regulator of G protein signaling 10 mRNA complete cds	
40387	7	H99460	Hs.108873	ESTs	
27236	7	AA417037	Hs.67805	ESTs	
20083	7	H99879	Hs.28029	ESTs Highly similar to EPIDERMAL GROWTH FACTOR PRECURSOR [Mus musculus]	
21561	7	R33245	Hs.23076	ESTs	
21223	7	R08175	Hs.110130	Homo sapiens chromosome 19 cosmid F22329	
13405	7	AA450118	Hs.25722	ESTs Weakly similar to KRUPPEL-RELATED ZINC FINGER PROTEIN 1 [Homo sapiens]	
34845	7	AA293420	Hs.95464	ESTs Moderately similar to transcription enhancer factor TEF1 [H.sapiens]	
15059	7	U53831	Hs.85280	Human interferon regulatory factor 7 (humirf7) mRNA complete cds	
1945	7	L25878	Hs.89649	Epoxide hydrolase 1 microsomal (xenobiotic)	
42648	7	W92150	Hs.79310	Human GAP SH3 binding protein mRNA complete cds	
20041	7	H97012	Hs.11050	ESTs Weakly similar to L8004.7 gene product [S.cerevisiae]	
7053	6	Z84721	Hs.75792	Hemoglobin alpha 1	
23843	6	T92561	Hs.110422	ESTs	
25815	6	AA149889	Hs.96200	ESTs Weakly similar to A-kinase anchor protein 95 AKAP95 [R.norvegicus]	
8473	6	AA437346	Hs.2967	SHB adaptor protein (a Src homology 2 protein)	
34618	6	AA282143	Hs.58094	H.sapiens mRNA for melanoma growth regulatory protein MIA	
11074	6	AA148983	Hs.29068	ESTs	
17533	6	AA127098	Hs.71057	EST	
28973	6	F04014	Hs.65996	ESTs	
17042	6	AA070397	EST - RC_AA070397	EST - RC_AA070397	
15246	6	W01094	Hs.84628	ESTs	
2247	6	M10321	Hs.110802	VON WILLEBRAND FACTOR PRECURSOR	
30810	6	N53419	Hs.47646	ESTs	
13348	6	AA449267	Hs.17914	ESTs Weakly similar to HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT [M.musculus]	
1789	6	L13258	Hs.936	Solute carrier family 17 (sodium phosphate) member 2	
16627	5	AA036779	Hs.61826	Homo sapiens clone 23928 mRNA sequence	

## FIGURE 6 (CONT.)

27103	5	AA0404282	Hs.63481	ESTs	Weakly similar to kynurenine/alpha-aminoadipate aminotransferase [R. norvegicus]
12631	5	AA412293	Hs.21258	ESTs	
11599	5	AA242829	Hs.7508	ESTs	
9010	5	C01360	Hs.67364	Homo sapiens clone 23904 mRNA sequence	
4660	5	U53225	Hs.75283	Sorting nexin 1	
5244	5	U85992	Hs.87197	Human clone IMAGE:35527 unknown protein mRNA partial cds	
7953	5	AA284403	Hs.74750	Homo sapiens mRNA for KIAA0554 protein partial cds	
27617	5	AA446114	Hs.55409	ESTs	
39480	5	D60419	Hs.81915	STATHMIN	
37529	5	AA456112	Hs.99410	ESTs	
11858	5	AA262308	Hs.105385	ESTs	
37294	5	AA450127	Hs.110571	ESTs	Highly similar to MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118 [Mus musculus]
23201	5	T40652	Hs.8279	ESTs	
28767	5	D45608	Hs.83792	Surfactant pulmonary-associated protein D	
3151	4	M83652	Hs.53155	Properdin P factor complement	
29196	4	H24456	Hs.85053	Homo sapiens clone 24440 mRNA sequence	
12863	4	AA425782	Hs.27973	ESTs	
42486	4	W68410	Hs.106857	Calbindin 2 (29kD calretinin)	
23571	4	T80628	Hs.103169	ESTs	
12376	4	AA399271	Hs.19610	ESTs	
27894	4	AA460319	Hs.48469	ESTs	
24935	4	AFFX-	AFFX-HUMGAPDH/M33197_M		
4238	4	U33053	Hs.2499	Human lipid-activated protein kinase PRK1 mRNA complete cds	
41844	4	T15833	Hs.100227	EST	
20111	4	N21380	Hs.25497	H. sapiens mRNA for ROX protein	
8316	4	AA410529	Hs.30732	ESTs	
39794	4	H21819	Hs.14896	Homo sapiens clone 24590 mRNA sequence	
1517	4	J04501	Hs.772	Glycogen synthase 1 (muscle)	
9164	4	D38081	Hs.89887	Thromboxane A2 receptor	
35027	4	AA349996	Hs.96937	ESTs	
14158	4	AA490182	Hs.118598	ESTs	
41950	4	T33137	Hs.7967	ESTs	
34360	4	AA251547	Hs.104358	EST	
6547	4	X95808	Hs.9568	Human mRNA for KIAA0385 gene complete cds	
20863	4	N69989	Hs.19167	ESTs	
12734	4	AA419200	Hs.5737	ESTs	
39497	4	D80154	Hs.56340	ESTs	
1600	4	K03474	EST - K03474		
27148	4	AA405231	Hs.100113	Human mRNA for KIAA0381 gene partial cds	
10763	4	AA057620	Hs.30807	ESTs	

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## FIGURE 6 (CONT.)

17007	4	AA069696	Hs.67317	ESTs	
13522	4	AA454115	Hs.6000	ESTs	
18444	4	AA232646	Hs.68061	ESTs	
27665	3	AA447759	Hs.134724	ESTs	
21382	3	R16896	Hs.89615	PROTEIN KINASE C THETA TYPE	
2052	3	L36818	Hs.75339	Inositol polyphosphate phosphatase-like protein 1 (51C protein)	
9039	3	C02049	Hs.106291	ESTs	
34888	3	AA303078	Hs.94479	Human GT334 protein (GT334) gene mRNA complete cds	
11047	3	AA142849	Hs.22660	ESTs	
19451	3	H23747	Hs.31697	ESTs	
2822	3	M55621	Hs.117946	N-acetylglucosaminyltransferase I	
13928	3	AA478441	Hs.11590	ESTs	
12064	3	AA283848	Hs.11367	ESTs Weakly similar to KIAA0009 [H.sapiens]	
3836	3	U12707	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	
4528	3	U48251	Hs.75871	Homo sapiens protein kinase C-binding protein RACK7 mRNA partial cds	
42064	3	T63364	Hs.9225	ESTs Highly similar to FIBRINOGEN-LIKE PROTEIN A PRECURSOR [Parastichopus parviniensis]	
4586	3	U50743	Hs.19520	Sodium/potassium ATPase gamma subunit	
4914	3	U67611	EST - U67611		
20168	3	N24106	Hs.2709	Cartilage linking protein 1	
24281	3	W79773	Hs.16511	ESTs	
19634	3	H44666	Hs.31597	ESTs	
10989	3	AA132366	Hs.8023	Homo sapiens mRNA for SPOP	
6587	3	X97748	EST - X97748		
14096	3	AA487558	Hs.8135	ESTs	
13350	3	AA449297	Hs.8944	ESTs Weakly similar to type 1 procollagen C-proteinase enhancer protein precursor [H.sapiens]	
33930	3	AA169539	Hs.95870	ESTs	
34215	3	AA233855	Hs.104252	UTROPHIN	
22509	3	R71393	Hs.29190	ESTs	
20065	3	H98657	Hs.27291	ESTs	
31091	3	N63076	Hs.138746	EST	
2493	3	M22919	Hs.77385	MYOSIN LIGHT CHAIN ALKALI SMOOTH-MUSCLE ISOFORM	
28913	3	F01560	Hs.22583	ESTs Highly similar to co-repressor protein [M.musculus]	
14323	3	AA596575	Hs.12851	ESTs	
34914	3	AA338729	Hs.133096	ESTs	
14236	3	AA496891	Hs.5011	ESTs Weakly similar to The ha1237 gene product is related to S.pombe rad21 gene product. [H.sapiens]	
24594	3	Z38804	Hs.22555	ESTs Highly similar to OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR [Bos taurus]	
22589	3	R79580	Hs.29874	ESTs	
22156	3	R52145	Hs.25894	ESTs	
16404	3	AA021284	Hs.60554	ESTs Moderately similar to sodium-calcium exchanger form 3 [R.norvegicus]	
29310	3	H66642	Hs.88729	ESTs	

## FIGURE 6 (CONT.)

9758	3	M26393	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
9806	2	M79462	Hs.69633	Probable transcription factor PML (alternative products)
19289	2	H16568	Hs.23748	ESTs
34031	2	AA192614	Hs.83577	Human LIM protein MLP mRNA complete cds
33299	2	W73790	Hs.73803	IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR
3276	2	M93718	Hs.76983	Nitric oxide synthase 3 (endothelial cell)
31704	2	N75055	Hs.14632	ESTs
10310	2	R87373	Hs.75429	ESTs
22388	2	R63695	Hs.1432	Protein kinase C substrate 80K-H
20938	2	N73988	Hs.37477	ESTs Weakly similar to No definition line found [C.elegans]
5935	2	X62466	Hs.108338	CDW52 antigen (CAMPATH-1 antigen)
41485	2	R49689	Hs.5260	ESTs Weakly similar to CD6G8.3 [C.elegans]
25403	2	AA063316	EST - RC_AA063316	EST - RC_AA063316
27965	2	AA464267	Hs.24912	Homo sapiens bicaudal-D (BICD) mRNA complete cds
40632	2	N45221	EST - RC_N45221	EST - RC_N45221
15527	2	W28798	Hs.63260	Phosphodiesterase 6A cGMP-specific rod alpha
31672	2	N74336	Hs.91681	ESTs
964	2	HG1804	EST - HG1804-HT1829	EST - HG1804-HT1829
12439	2	AA401452	Hs.32060	ESTs
24223	2	W70158	Hs.29696	ESTs
21052	2	N93764	Hs.10175	ESTs Weakly similar to hypothetical protein [H.sapiens]
34140	2	AA215637	Hs.104186	ESTs
5130	2	U79288	Hs.85053	Homo sapiens clone 24440 mRNA sequence
30041	2	N27628	Hs.132744	Homo sapiens clone 24525 mRNA sequence
19202	2	H11509	Hs.22482	ESTs
41350	2	R40442	Hs.75652	Glutathione S-transferase M5
914	2	HG1019	EST - HG1019-HT1019	EST - HG1019-HT1019
31958	2	N93495	Hs.54960	ESTs
12014	2	AA281769	Hs.7214	Human Hpast (HPAST) mRNA complete cds
39777	2	H18412	Hs.75253	Human clone ID 193225 NAD (H)-specific isocitrate dehydrogenase gamma subunit mRNA alternatively spliced partial cds
19147	2	H09751	Hs.117619	ESTs
11199	2	AA176446	Hs.10024	ESTs
6477	2	X91504	Hs.64904	Transcription factor COUP 2 (a.k.a. ARP1)
16336	2	AA018601	Hs.75649	EXTRACELLULAR SIGNAL-REGULATED KINASE 3
24058	2	W23709	Hs.109047	ESTs
26180	2	AA251230	Hs.112272	ESTs
37177	2	AA447988	Hs.7765	ESTs
41894	2	T47601	Hs.138805	ESTs
36532	2	AA429889	Hs.68882	Acrosin
1450	2	J03071	Hs.115352	Growth hormone 1

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## FIGURE 6 (CONT.)

24819	2	Z40923	Hs.24812	ESTs	
6532	2	X95325	Hs.89491	DNA-BINDING PROTEIN A	
27085	2	AA402495	Hs.77978	ESTs	
20487	2	N52322	Hs.19978	ESTs	
724	2	D83703	Hs.30729	Peroxisomal biogenesis factor 6	
4132	2	U27655	Hs.82294	Human RGP3 mRNA complete cds	
13375	2	AA449716	Hs.5723	ESTs	
13988	2	AA480045	Hs.7934	ESTs	
22306	2	R59006	Hs.100630	ESTs	
23187	2	T33184	Hs.12840	Homo sapiens gemtine mRNA sequence	
11320	2	AA213667	Hs.22222	ESTs	
24608	2	Z38888	Hs.25046	ESTs	
13163	2	AA437225	Hs.22410	ESTs	
1139	2	HG3227-		EST - HG3227-HT3404	
35572	2	AA401489		EST - RC_AA401489	
6964	2	Z49105	Hs.137591	H.sapiens HD21 mRNA	
30963	2	N59373	Hs.26812	ESTs	
16164	2	AA007509	Hs.75395	Human mRNA for TPRD complete cds	
2174	2	L42611	Hs.111758	KERATIN TYPE II CYTOSKELETAL 6D	
38958	2	AA609707	Hs.112751	ESTs	
37919	2	AA478162	Hs.104965	ESTs	
28905	2	D81123	Hs.57475	ESTs	
3745	2	U09117	Hs.80776	Human phospholipase c delta 1 mRNA complete cds	
19545	2	H37834	Hs.32699	ESTs	
8416	2	AA428531		EST - AA428531	
17569	2	AA128926		EST - RC_AA128926	
19354	2	H18829	Hs.121515	ESTs	
7598	2	AA174185	Hs.3354	Homo sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA complete cds	
25385	2	AA059099	Hs.109727	ESTs	
14176	2	AA490620	Hs.11809	ESTs	
29487	2	H85120	Hs.80881	N-ACETYLLACTOSAMINE SYNTHASE	
10197	2	R64199	Hs.50785	Homo sapiens vesicle trafficking protein sec22b mRNA complete cds	
19488	2	H27675	Hs.25804	ESTs	
10568	2	AA029703	Hs.36574	ESTs	
30798	2	N53143	Hs.64001	ESTs	
9638	2	L07592	Hs.106415	Human peroxisome proliferator activated receptor mRNA complete cds	
27195	2	AA411473	Hs.65311	ESTs	
17438	2	AA115508	Hs.2780	Jun D proto-oncogene	
24932	2	AFFX-		AFFX-HSAC07X00351_M	
10944	2	AA125969	Hs.34769	ESTs Weakly similar to F35G12.9 [C.elegans]	

## FIGURE 6 (CONT.)

42324	2	T88199	Hs.142702	ESTs	
34756	2	AA287665	Hs.8245	ESTs	
12743	2	AA421050	Hs.24545	ESTs	
13676	2	AA459389	Hs.26350	Homo sapiens mRNA for tyrosyl sulfotransferase-2	
13009	2	AA430474	Hs.16466	ESTs	
7403	2	AA094921	Hs.79788	ESTs	
35689	2	AA404707	Hs.54865	ESTs	
17701	2	AA135941	Hs.71626	ESTs	
18713	2	F04686	Hs.21782	ESTs	
8314	2	AA410355	Hs.103081	ESTs Highly similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens]	
7990	2	AA291786	Hs.32822	ESTs Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]	
42791	2	AFEX-		AFEX-HUMGAPDH433197_M	
6893	1	Z30643	Hs.123123	H.sapiens mRNA for chloride channel (putative) 2139bp	
35607	1	AA402267	Hs.133475	ESTs Weakly similar to zinc finger protein [H.sapiens]	
9468	1	H46074	Hs.31562	ESTs	
29469	1	H82929		EST - RC_H82929	
18692	1	F04444	Hs.6217	ESTs	
35205	1	AA398161	Hs.37602	ESTs	
22184	1	R53520	Hs.102755	ESTs	
28915	1	D59267	Hs.56782	ESTs	
17913	1	AA151480	Hs.91202	ESTs	
24655	1	Z39191	Hs.27262	ESTs Weakly similar to Lph17p [S.cerevisiae]	
15811	1	W51743	Hs.35096	ESTs	
15700	1	W73859	Hs.78061	Homo sapiens mesoderm-specific basic-helix-loop-helix protein (POD1) mRNA complete cds	
36770	1	AA435753		EST - RC_AA435753	
32400	1	R97176	Hs.110783	ESTs	
10802	1	AA069425	Hs.20573	ESTs	
17593	1	AA129856		EST - RC_AA129856	
20266	1	N32118	Hs.107365	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]	
14447	1	AA609045	Hs.11759	ESTs	
12852	1	AA426521	Hs.18528	Homo sapiens mRNA for NA14 protein	
19738	1	H53059	Hs.15548	ESTs	
14471	1	AA609346	Hs.20102	ESTs	
5796	1	X55019	Hs.98975	Cholinergic receptor nicotinic delta polypeptide	
18441	1	AA232508	Hs.77480	ESTs	
10164	1	R54743	Hs.19400	ESTs Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]	
8830	1	AB002319	Hs.8663	Human mRNA for KIAA0321 gene partial cds	
8682	1	AA477891	Hs.104476	ESTs	
35620	1	AA402493	Hs.10552	ESTs Highly similar to c-Jun leucine zipper interactive [M.musculus]	
35401	1	AA399593	Hs.97682	EST	

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## FIGURE 6 (CONT.)

10901	1	AA112307	Hs.25224	ESTs	
19546	1	H37901	Hs.32706	ESTs	
30292	1	N35978	Hs.82364	ESTs	
39087	1	AA620607	Hs.111591	ESTs	
37896	1	AA477463	Hs.77039	Ribosomal protein S28	
41552	1	R59352	Hs.101253	Human mRNA for KIAA0296 gene complete cds	
11467	1	AA234089	Hs.14593	ESTs	
8215	1	AA389673	Hs.84344	ESTs Weakly similar to No definition line found [C.elegans]	
15505	1	W28366	Hs.7252	Homo sapiens clone 24800 mRNA sequence	
9834	1	M92299	Hs.22554	Homoio box BS (2.1 protein)	
9159	1	D31483	Hs.90062	Homo sapiens clone 23565 unknown mRNA partial cds	
42218	1	T86444	Hs.110095	ESTs	
15526	1	W28790	Hs.8124	ESTs	
17790	1	AA150182	Hs.42262	ESTs Weakly similar to HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III [C.elegans]	
9777	1	M57888	Hs.95946	GRANZYME H PRECURSOR	
15373	1	W26376	Hs.74563	THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR	
12076	1	AA284362	Hs.6448	ESTs Weakly similar to No definition line found [C.elegans]	
15391	1	W26651	Hs.15961	ESTs	
12905	1	AA427537	Hs.32419	ESTs	
39820	1	H24085	Hs.25443	ESTs	
13109	1	AA435838	Hs.7985	ESTs	
24249	1	W73069	Hs.12600	ESTs	
16514	1	AA027946	Hs.44608	ESTs	
16767	1	AA046850	Hs.40342	ESTs	
15381	1	W26496	Hs.107725	ESTs Weakly similar to LIS-1 protein [H.sapiens]	
11690	1	AA252762	Hs.31235	ESTs	
22989	1	T16510	Hs.6624	ESTs	
24490	1	Z38153	Hs.26921	ESTs	
24368	1	W87280	Hs.124800	ESTs	
22565	1	R77631	Hs.29126	ESTs	
15358	1	W26105	Hs.8961	ESTs	
24186	1	W61319	Hs.37482	ESTs Highly similar to COATOMER ZETA SUBUNIT [Bos taurus]	
22272	1	R58922	Hs.26580	ESTs	
16434	1	AA024494	Hs.61199	ESTs	
22692	1	R88711	Hs.34183	ESTs	
38830	1	AA609189	Hs.116415	ESTs	
42547	1	W73946		EST - RC_W73946	
34885	1	AA302831	Hs.57732	Homo sapiens p38beta2 MAP kinase mRNA complete cds	
18445	1	AA232648	Hs.87088	ESTs	
18070	1	AA180352	Hs.72733	ESTs	

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**FIGURE 6 (CONT.)**

23923 1 T96407 Hs.17812 ESTs

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## FIGURE 7

Primary Key	fold downregulated of Tumor vs	Accession	Unigene CLUSTER	Unigene Descriptor
2348	>10	M15656	Hs.75592	Aldolase B fructose-bisphosphate
6463	>10	X90908	Hs.74126	H.sapiens mRNA for L-15P (L-BABP) protein
42139	>10	T73335	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
4544	>10	U48959	Hs.75950	H.sapiens mRNA for myosin light chain kinase
1583	>10	K02765	Hs.56512	COMPLEMENT C3 PRECURSOR
2426	>10	M18828	Hs.385	Apolipoprotein B (including Ag(x) antigen)
8859	>10	AB002351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z38688	Hs.24192	ESTs
17810	>10	AA151402	Hs.46531	ESTs
7006	>10	Z70295	Hs.32966	H.sapiens mRNA for GCAP-III/uroguanylin precursor
1304	>10	HG4310	EST - HG4310-HT4580	
5980	>10	X64559	Hs.65424	Tetranectin (plasminogen-binding protein)
41987	>10	T47089	Hs.121713	Cytochrome P450 subfamily XXI (steroid 21-hydroxylase congenital adrenal hyperplasia)
24461	>10	W94427	Hs.3807	ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus musculus]
2372	>10	M16594	Hs.89552	Glutathione S-transferase A2
6001	>10	X65727	Hs.89552	Glutathione S-transferase A2
1750	>10	L10955	Hs.89485	Carbonic anhydrase IV
15130	>10	U77643	Hs.95655	Homo sapiens K12 protein precursor mRNA complete cds
12467	>10	AA402656	Hs.28264	ESTs
41148	>10	R06984	EST - RC_R06984_s	
31852	>10	N73958	Hs.50404	Human chemokine (TECK) mRNA complete cds
23483	>10	T68873	Hs.143289	H.sapiens mRNA for metallothionein isoform 1R
4605	>10	U51010	EST - U51010	
28359	>10	AA609133	Hs.58115	ESTs
24066	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194	Hs.89552	ESTs
12084	>10	AA284767	Hs.21910	ESTs
41473	>10	R48732	Hs.11006	ESTs
32568	>10	T29248	Hs.143113	Human pancreatic lipase related protein 2 (PLRP2) mRNA complete cds
6413	>10	X87159	Hs.37129	Sodium channel nonvoltage-gated 1 beta (Liddle syndrome)
20707	>10	N64436	Hs.20813	ESTs
27108	>10	AA404397	Hs.58414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
12477	>10	AA403032	Hs.21701	ESTs
42059	>10	T61654	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
25466	>10	AA079072	Hs.1477	Insulin-like growth factor binding protein 6
26910	>10	AA303081	Hs.78293	ESTs

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## FIGURE 7 (CONT.)

16938	>10	AA059473	Hs.66783	ESTs	
41788	>10	T03735	Hs.26885	ESTs	
7754	>10	AA234634	Hs.76722	Human NF-IL6-beta protein mRNA complete cds	
6122	>10	X72012	Hs.75962	Endoglin (Osler-Rendu-Weber syndrome 1)	
2848	>10	M58286	Hs.159	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR	
23013	>10	T16661	Hs.6725	ESTs	
19537	>10	H30270	Hs.32583	ESTs	
4584	>10	U50360	EST - U50360	EST - U50360	
37410	>10	AA453652	Hs.99344	ESTs	
27969	>10	AA464594	Hs.63382	ESTs	
35497	>10	AA400606	Hs.144344	EST	
37013	>10	AA443690	Hs.136268	ESTs	
39247	>10	AA621553	Hs.112998	ESTs	ESTs Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]
13471	>10	AA452598	Hs.109590	ESTs	
42110	>10	T68878	Hs.76688	Carboxylesterase 2 (liver)	
10965	>10	AA128997	Hs.18953	Human sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA complete cds	
4918	>10	U67733	Hs.3831	Human cGMP-stimulated 3'-cyclic nucleotide phosphodiesterase PDE2A3 (PDE2A) mRNA complete cds	
40737	>10	N54950	Hs.81454	H.sapiens KHK mRNA for ketohexokinase done pHKK3a	
30403	>10	N45300	Hs.110647	Meis1 (mouse) homolog	
11432	>10	AA233369	Hs.361	ESTs	
18784	>10	F09748	Hs.7974	ESTs	
40662	>10	N49281	EST - RC_N49281	EST - RC_N49281	
5773	>10	X54162	Hs.79386	64 KD AUTOANTIGEN D1	
35041	>10	AA350586	Hs.30862	ESTs	
20868	>10	N70068	Hs.7243	ESTs	
39729	>10	H11489	Hs.105805	ESTs	
27387	>10	AA426330	Hs.78264	ESTs	
39758	>10	H15814	Hs.80485	Human apM1 mRNA for GS3109 (novel adipose specific collagen-like factor) complete cds	
4319	>10	U37283	Hs.58882	Human microfibril-associated glycoprotein-2 MAGP-2 mRNA complete cds	
2866	>10	M59815	Hs.76682	Complement component 4A	
30332	>10	N39075	Hs.44934	EST	
41344	>10	R40189	Hs.6985	ESTs	
28271	>10	AA521200	Hs.48778	ESTs	
5834	>10	X57129	Hs.7644	HISTONE H1D	
19048	>10	H05464	Hs.100251	ESTs	
1429	>10	J02854	Hs.9615	Human 20-kDa myosin light chain (MLC-2) mRNA complete cds	
19491	>10	H27910	Hs.107384	ESTs	
25992	>10	N26386	Hs.33084	Solute carrier family 2 (facilitated glucose transporter) member 5	
2041	>10	L36033	Hs.77423	Stromal cell-derived factor 1	
22865	>10	R99909	Hs.36186	ESTs	

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## FIGURE 7 (CONT.)

11624	>10	AA243654	Hs.17998	ESTs	
12512	>10	AA405199	Hs.20733	ESTs	
41443	>10	R45577	Hs.10683	ESTs	
5055	>10	U77180	Hs.50002	Human mRNA for EBI1-ligand chemokine complete cds	
6038	>10	X66945	Hs.748	Basic fibroblast growth factor (bFGF) receptor (shorter form)	
42530	>10	W72859	Hs.74669	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]	
827	>10	D87433	Hs.84753	Human mRNA for KIAA0246 gene partial cds	
650	>10	D78014	Hs.74566	Human mRNA for dihydropyrimidinase related protein-3 complete cds	
37350	>10	AA452606	Hs.99289	EST	
37486	>10	AA455178	Hs.99397	ESTs	
36846	>10	AA431797	Hs.98763	EST - RC_AA609907	
38999	>10	AA609907		ESTs	
38191	>10	AA487895	Hs.17311	ESTs	
9944	>10	N57484	Hs.74670	Human mRNA for KIAA0146 gene partial cds	
8139	>10	AA341723	Hs.107374	ESTs	
41522	>10	R53966	Hs.75092	N-CHIMAERIN	
38090	>10	AA482603	Hs.111301	Matrix metalloproteinase 2 (gelatinase A 72kD gelatinase 72kD type IV collagenase)	
41175	>10	R09241		EST - RC_R09241	
36947	>10	AA437388	Hs.115726	ESTs	
4175	>10	U29653	Hs.76110	Pigment epithelium-derived factor	
35421	>10	AA389886	Hs.97669	EST	
4358	>10	U39487	Hs.250	Xanthine dehydrogenase	
35463	>10	AA400272	Hs.97758	EST	
7026	>10	Z80345	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain	
34625	>10	AA282238	Hs.118463	Homo sapiens clone 24519 unknown mRNA partial cds	
20179	>10	N24879	Hs.9693	ESTs	
36805	>10	AA435901	Hs.56874	ESTs Weakly similar to p20 protein [R.norvegicus]	
24447	>10	W93121	Hs.23841	Human mRNA for KIAA0355 gene complete cds	
10247	>10	R74386	Hs.108924	ESTs	
3618	>10	U02388	Hs.101	Leukotriene B4 omega hydroxylase (cytochrome P450 subfamily VF)	
18730	>10	F08876	Hs.8008	ESTs	
22529	>10	R73075	Hs.29327	EST	
37520	>10	AA455960	Hs.99405	ESTs	
41122	>10	R05463	Hs.138500	ESTs	
4417	>10	U42031	Hs.7557	Human 54 kDa progesterone receptor-associated immunophilin FKBP54 mRNA partial cds	
9742	>10	M14777	Hs.89552	Glutathione S-transferase A2	
36194	>10	AA421142	Hs.104672	ESTs	
4445	>10	U43653	Hs.3261	Leptin (murine obesity homolog)	
19749	>10	H53728	Hs.36808	ESTs	
19793	>10	H56965	Hs.34564	ESTs	

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## FIGURE 7 (CONT.)

12713	>10	AA418398	Hs.17778	ESTs	
1464	>10	J03474	Hs.3157	SERUM AMYLOID A PROTEIN PRECURSOR	
16842	>10	AA055163	Hs.57975	Homo sapiens mRNA for cardiac caldesmon complete cds	
34229	>10	AA234383	Hs.3576	ESTs	
35563	>10	AA401404	Hs.112087	ESTs	
16736	>10	AA045306	Hs.42996	ESTs	
33607	>10	W83497	Hs.59486	ESTs	
16146	>10	AA005236	Hs.60162	ESTs	
22666	>10	R65880	Hs.33455	ESTs	
22562	>10	R77493	Hs.29653	EST	
22985	>10	T16211	Hs.6326	Homo sapiens clone 23798 and 23825 mRNA sequence	
5248	>10	U86358	Hs.50404	Human chemokine (TECK) mRNA complete cds	
27608	>10	AA443800	Hs.43125	ESTs	
7510	>10	AA136353	Hs.38022	ESTs	
34683	>10	AA284920	Hs.13716	ESTs	
27633	>10	AA446659	Hs.2563	Tachykinin 2 (substance K neurokinin A neurokinin 2 neurokinin L neurokinin alpha neuropeptide K neuropeptide gamma)	
32485	>10	T16335	Hs.65325	EST	
38791	>10	AA609018	Hs.112629	ESTs	
32020	>10	N95796	Hs.55181	ESTs	
19986	>10	H99980	Hs.12112	ESTs Moderately similar to protein phosphatase 1 binding protein PTG [M.musculus]	
30748	>10	N52254	Hs.47438	ESTs	
8903	>10	AF002246	Hs.21226	Homo sapiens neural cell adhesion molecule (CALL) mRNA complete cds	
9959	>10	N75215	Hs.43148	ESTs	
38136	>10	AA486185	Hs.125176	ESTs	
19845	>10	H59887	Hs.35167	ESTs	
1127	>10	HG3117-	EST - HG3117-HT3293		
23637	>10	T85315	Hs.15903	ESTs	
16699	>10	AA043349	Hs.62630	ESTs	
36702	>10	AA434108	Hs.101393	ESTs Moderately similar to DNAJ PROTEIN HOMOLOG 1 [Homo sapiens]	
28930	>10	F02702	Hs.141503	Small inducible cytokine A5 (RANTES)	
9226	>10	D62584	Hs.109439	ESTs Highly similar to OSTEOINDUCTIVE FACTOR PRECURSOR [Bos taurus]	
3357	>10	M99487	Hs.1915	PROSTATE-SPECIFIC MEMBRANE ANTIGEN	
36783	>10	AA435805	Hs.112065	EST	
4876	>10	U66061	Hs.2048	Protease serine 2 (trypsin 2)	
41149	>10	R08986	Hs.76487	ESTs	
22200	>10	R54179	Hs.26100	ESTs	
15925	>10	Y13492	Hs.78483	Homo sapiens mRNA for smoothelin	
10911	>10	AA113387	Hs.24305	ESTs	
3336	>10	M97675	Hs.1944	Human protein tyrosine kinase l-Ror1 (Ror1) mRNA complete cds	
31889	>10	N91897	Hs.50652	ESTs	

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FIGURE 7 (CONT.)

10406	>10	AA007629	Hs.25476	ESTs	
17737	>10	AA142875	Hs.71718	ESTs	
36939	>10	AA609632	Hs.112737	EST	
16206	>10	AA010611	Hs.60418	EST	
32810	>10	W15376	Hs.122656	ESTs	
18210	>10	AA196306	Hs.86045	ESTs	
24054	>10	W15580	Hs.15342	ESTs	
23047	>10	T23457	Hs.7120	ESTs	
12944	>10	AA428258	Hs.8769	ESTs	
34172	>10	AA227469	Hs.139171	EST	
9317	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds	
19331	>10	H17865	Hs.23213	ESTs	
21035	>10	N92824	Hs.14898	ESTs	
34208	>10	AA233380	Hs.104249	EST	
5974	>10	X64072	Hs.83968	Integrin beta 2 (antigen CD18 (p95) lymphocyte function-associated antigen 1 macrophage antigen 1 (mac-1) beta subunit)	
5032	>10	U74382	Hs.90357	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds	
41941	>10	T32561	Hs.5476	ESTs	
34239	>10	AA235009	Hs.32246	ESTs	
32852	>10	W31906	Hs.116428	ESTs	
7662	>10	AA203527	Hs.18747	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds	
6432	>10	X89066	Hs.94413	Transient receptor potential channel 1	
37001	>10	AA443311	Hs.98998	ESTs	
4630	>10	U52101	Hs.9999	Human YMP mRNA complete cds	
19489	>10	H27852	Hs.28137	ESTs	
28483	>10	C14270	Hs.66357	ESTs	
19801	>10	H57357	Hs.18767	ESTs Weakly similar to unknown protein [H.sapiens]	
24672	>10	Z39300	Hs.124952	ESTs	
31153	>10	N63688		EST - RC_N63688	
40250	>10	H92451	Hs.110	Solute carrier family 3 (cystine dibasic and neutral amino acid transporters activator of cystine dibasic and neutral amino acid transport) member 1	
23028	>10	T17215	Hs.6952	ESTs	
28072	>10	AA400886	Hs.86693	ESTs	
11868	>10	AA262556	Hs.28802	ESTs Weakly similar to centaurin alpha [R.norvegicus]	
35359	>10	AA399061	Hs.112961	ESTs Moderately similar to PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR [H.sapiens]	
4285	>10	U35139	Hs.50130	Human NECDN related protein mRNA complete cds	
4655	>10	U52969	Hs.80296	BRAIN SPECIFIC POLYPEPTIDE PEP-19	
26030	>10	AA235984	Hs.87469	ESTs	
2042	>10	L36051	Hs.1166	Thrombopoietin (myeloproliferative leukemia virus oncogene ligand megakaryocyte growth and development factor)	
25262	>10	AA043501	Hs.30250	Homo sapiens short form transcription factor C-MAF (c-maf) mRNA complete cds	
34821	>10	AA291983	Hs.144599	ESTs	
42405	>10	W44682	Hs.109896	ESTs	

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## FIGURE 7 (CONT.)

41248	>10	R40395	Hs.112125	Lecithin-cholesterol acyltransferase
14494	>10	AA609845	Hs.25632	ESTs Weakly similar to PNG gene [H.sapiens]
4453	>10	U43916	Hs.78368	Human epithelial membrane protein (CL-20) mRNA complete cds
42758	>10	Z41411	Hs.107040	ESTs
2098	>10	L39009	EST - L39009	EST - L39009
35637	>10	AA402933	Hs.29283	ESTs
16549	>10	AA029697	Hs.94854	ESTs
1220	>10	HG3733-	HG3733-HT4003	EST - HG3733-HT4003
39934	>10	H52185	Hs.124994	ESTs
7735	>10	AA232121	Hs.109631	Human tyrosyl-tRNA synthetase mRNA complete cds
40392	>10	H99587	Hs.108880	ESTs
37170	>10	AA447779	Hs.99145	EST
18361	>10	AA223902	Hs.96899	ESTs
19366	>10	H19204	Hs.133466	ESTs
38429	>10	AA496965	Hs.108694	Glycophorin A
38021	>10	AA481059	Hs.105152	ESTs
5184	>10	U82169	Hs.87234	Human frizzled homolog (FZD3) mRNA complete cds
27863	>10	AA458923	Hs.70202	ESTs Weakly similar to F23B2.4 [C.elegans]
37476	>10	AA455051	Hs.99386	EST
859	>10	D87468	Hs.40888	Human mRNA for KIA0278 gene partial cds
27185	>10	AA410895	Hs.62348	ESTs
41010	>10	N80686	Hs.21639	Human APEG-1 mRNA complete cds
38241	>10	AA489076	Hs.105101	ESTs
22701	>10	R89477	Hs.34299	ESTs
12152	>10	AA291271	Hs.10886	ESTs Weakly similar to uroporphyrinogen III synthase UROIIIH [H.sapiens]
38913	>10	AA609531	Hs.112050	ESTs
34034	>10	AA192871	Hs.63760	Troporin I (skeletal fast)
37644	>10	AA459857	Hs.99503	EST
4173	>10	U29725	Hs.3080	Human BMK1 alpha kinase mRNA complete cds
16178	>10	AA009839	Hs.1632	CD27L RECEPTOR PRECURSOR
20527	>10	N54161	Hs.124044	ESTs
41918	>10	T25873	Hs.102243	ESTs
1525	>10	J04621	Hs.1501	Syndecan 2 (heparan sulfate proteoglycan 1 cell surface-associated fibroglycan)
19160	>10	H10208	Hs.30972	EST
16860	>10	AA055833	Hs.58152	ESTs Weakly similar to Natsv [M.musculus]
36927	>10	AA437259	Hs.104944	EST
1595	>10	K03207	Hs.103972	Salivary proline-rich protein
15574	>10	W38778	Hs.25216	ESTs
8985	>10	C00125	Hs.24332	ESTs Weakly similar to deoxyribose-phosphate aldolase [C.elegans]
33995	>10	AA182845	Hs.139088	Homo sapiens FIP2 alternatively translated mRNA complete cds

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## FIGURE 7 (CONT.)

7949	>10	AA283620	Hs.34956	ESTs	
16607	>10	AA034918	Hs.85079	ESTs	
11670	>10	AA252191	Hs.25199	Homo sapiens PAC clone DJ130H16 from 22q12.1-qter	
7354	>10	AA092348	Hs.7858	ESTs	
4277	>10	U34879	Hs.65279	ESTRADIOL 17 BETA-DEHYDROGENASE 1	
23214	>10	T40895	Hs.11937	Human protein tyrosine phosphatase PTPCAAX1 (PTPCAAX1) mRNA complete cds	
22209	>10	RS4594	Hs.25209	ESTs	
36151	>10	AA419011	Hs.96744	ESTs	
23372	>10	T59537		EST - RC_T59537	
42136	>10	T72491	Hs.73849	Apolipoprotein C-III	
289	>10	D16480	Hs.75860	Hydroxacyl-Coenzyme A dehydrogenase/3-ketocyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein) alpha subunit	
15974	>10	Z36531	Hs.2659	H.sapiens mRNA for fibrinogen-like protein (pT49 protein)	
41379	>10	R42233	Hs.106487	Homo sapiens mRNA for KIAA0673 protein partial cds	
34764	>10	AA287870	Hs.890	Lymphotoxin-beta	
24027	>10	W01875	Hs.5734	Homo sapiens mRNA for KIAA0679 protein partial cds	
36197	>10	AA421158	Hs.97514	ESTs	
37211	>10	AA448334		EST - RC_AA448334	
27684	>10	AA448625	Hs.57929	ESTs	
31790	>10	N80279	Hs.50891	ESTs	
24515	>10	Z38289	Hs.12701	ESTs	
18652	>10	F03111	Hs.22505	ESTs	
16635	>10	AA037433	Hs.46987	ESTs	
37815	>10	AA469952	Hs.97899	ESTs	
9034	>10	X83857	Hs.495	Prostaglandin E receptor 3 (subtype EP3) (alternative products)	
16469	>10	C01833	Hs.29759	ESTs Weakly similar to Hs.495	
27034	>10	AA025728	Hs.61307	ESTs	
42746	>10	AA400102	Hs.49051	ESTs	
35368	>10	Z40646	Hs.124953	ESTs	
34805	>10	AA291522	Hs.97250	Homo sapiens DBI-related protein mRNA complete cds	
19983	>10	H89355	Hs.6598	ESTs	
31126	>10	N63444	Hs.47566	ESTs	
22616	>10	R81949	Hs.124964	ESTs	
12246	>10	AA348198	Hs.14829	Homo sapiens mRNA for GABA-BR1a (hGB1a) receptor	
8777	>10	AA495865	Hs.7974	ESTs	
13486	>10	AA453034	Hs.21041	ESTs Highly similar to FIBROPELLIN C PRECURSOR [Strongylocentrotus purpuratus]	
25512	>10	AA085721	Hs.95511	ESTs	
29073	>10	F12567		EST - RC_F12567	
5541	>10	X07203	Hs.89751	CD20 RECEPTOR	
41689	>10	R82942	Hs.107755	ESTs Weakly similar to GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE [E.coli]	

## FIGURE 7 (CONT.)

32343	>10	R60965	Hs.125052	ESTs	
38335	>10	AA490916	Hs.112157	ESTs	
41729	>10	R92458	Hs.89554	Hemoglobin gamma-G	
36707	>10	AA434246	Hs.98802	EST	
28491	>10	C14784	Hs.12382	ESTs	
41702	>10	R86970	Hs.123363	ESTs	
32246	>10	R52163	Hs.144528	ESTs	
17314	>10	AA086487	Hs.107365	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC (Homo sapiens)	
30325	>10	N38967	Hs.44904	EST	
19823	>10	H58692	Hs.9520	ESTs Highly similar to FORMYL-TETRAHYDROFOLATE DEHYDROGENASE [Rattus norvegicus]	
42153	>10	T77729	Hs.89890	Pyruvate carboxylase	
19321	>10	H17511	Hs.24963	ESTs	
27110	>10	AA404494	Hs.84112	CTP synthetase	
28831	>10	D59722	Hs.92924	ESTs	
6333	>10	X82494	Hs.2653	Fibulin 2	
37679	>10	AA460661	Hs.99582	ESTs	
40829	>10	N64344	Hs.78362	Human clone 23839 mRNA sequence	
19132	>10	H09343	Hs.27261	ESTs	
19353	>10	H18706	Hs.31604	ESTs	
10935	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]	
11621	>10	AA243574	Hs.14691	ESTs	
38538	>10	AA521370	Hs.104423	ESTs	
10095	>10	R22139	Hs.30343	ESTs	
30014	>10	N26740	Hs.42771	ESTs	
4454	>10	U44429	Hs.16611	Human D53 (hD53) mRNA partial cds	
3650	>10	U03877	Hs.76224	Human extracellular protein (S1.5) mRNA complete cds	
36377	>10	AA426056	Hs.98450	ESTs	
20437	>10	N50550	Hs.24587	Homo sapiens mRNA for Eis1 complete cds	
1576	>10	K02100	Hs.117050	ORNITHINE CARBAMOYL TRANSFERASE PRECURSOR	
42078	>10	T64891	Hs.144323	ESTs	
27257	>10	AA418001	Hs.46146	ESTs Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]	
30582	>10	N49848	Hs.46974	EST	
3631	>10	U03090	Hs.290	Homo sapiens Ca2+-dependent phospholipase A2 mRNA complete cds	
19026	>10	H04768	Hs.30484	ESTs	
4752	>10	U59632	Hs.3847	Glycoprotein Ib (platelet) beta polypeptide	
3786	>10	U09579	Hs.74984	CYCLIN-DEPENDENT KINASE INHIBITOR 1	
1437	>10	J02923	Hs.76506	Lymphocyte cytosolic protein 1 (L-plastin)	
33905	>10	AFX-		AFX-Tpox-5	
4310	>10	U37055	Hs.78034	Macrophage stimulating 1 (hepatocyte growth factor-like)	
25923	>10	AA342302	Hs.55036	ESTs	



## FIGURE 7 (CONT.)

5520	>10	X06256	Hs.119218	Integrin alpha 5 (fibronectin receptor alpha polypeptide)
37571	>10	AA457409	Hs.99458	EST
38800	>10	AA609052	Hs.112636	EST
27952	>10	AA463700	Hs.47042	Homo sapiens CD39L3 (CD39L3) mRNA complete cds
27621	>10	AA446242	Hs.56589	ESTs
38784	>10	AA608988	Hs.2051	Testis specific protein Y-linked
291	>10	D16532	Hs.73729	Very low density lipoprotein receptor
18014	>10	AA173168	Hs.57672	ESTs Weakly similar to myosin heavy chain [C.elegans]
16720	>10	AA044732	Hs.77208	ESTs
25336	>10	AA053405	Hs.101404	ESTs
2547	>10	M25809	Hs.1009	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 56/58kD isoform 1
39953	>10	H56010	Hs.108144	ESTs Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]
13777	>10	AA463504	Hs.6052	ESTs
13419	>10	AA450336	Hs.22269	ESTs
1403	>10	J00123	Hs.93557	PROENKEPHALIN A PRECURSOR
42373	>10	W35362	Hs.103012	ESTs
21520	>10	R28267	Hs.24258	ESTs
9796	>10	M63509	Hs.73974	Glutathione S-transferase M2 (muscle)
35650	>10	AA404271	Hs.22631	Human glutamate receptor (GLUR5) mRNA complete cds
42501	>10	W69586	Hs.103156	ESTs
33812	>10	Z41239	Hs.106960	ESTs
42473	>10	W63731	Hs.122531	ESTs
25195	>10	AA033780	Hs.75736	Apolipoprotein D
28607	>10	C21481	Hs.84630	ESTs Moderately similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]
3712	>10	U07620	Hs.89661	Human MAP kinase mRNA complete cds
6214	>10	X77307	Hs.2507	5-HYDROXYTRYPTAMINE 2B RECEPTOR
23575	>10	T80833	Hs.14794	ESTs
31775	>10	N79765	Hs.50847	ESTs
5206	>10	U82979	Hs.67846	Human clone HM18 monocytic inhibitory receptor precursor mRNA complete cds
22769	>10	R94521	Hs.124693	ESTs
9377	>10	H12674	Hs.9396	ESTs
29268	>10	H61046	Hs.70405	EST Moderately similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]
11061	>10	AA147537	Hs.4811	ESTs
41960	>10	T33511	Hs.4844	ESTs
29416	>10	H77734	Hs.36702	Homo sapiens roundabout 1 (robot1) mRNA complete cds
38248	>10	AA489218	Hs.105229	ESTs
37256	>10	AA449424	Hs.98428	ESTs
21911	>10	R43980	Hs.26320	ESTs
23184	>10	T34622	Hs.8108	ESTs Weakly similar to HYPOTHETICAL 35.8 KD PROTEIN IN PRP16-SRP40 INTERGENIC REGION [S.cerevisiae]
16225	>10	AA011305	Hs.10029	Cathepsin C

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## FIGURE 7 (CONT.)

27766	>10	AA453656	Hs.89417	ESTs	
16071	>10	AA001426	Hs.40863	ESTs	
17343	>10	AA100152	Hs.5921	ESTs	
10643	>10	AA040154	Hs.32478	ESTs	
29335	>10	H68239	Hs.39122	ESTs	
34966	>10	AA344866	Hs.1285	Complement component 8 gamma polypeptide	
26303	>10	AA255483	Hs.88042	EST	
1030	>10	HG2416-		EST - HG2416-IT2512	
28370	>10	AA609559	Hs.38550	ESTs Moderately similar to alfa subunit [H.sapiens]	
29303	>10	H65881	Hs.38427	ESTs	
21076	>10	N99976	Hs.8016	ESTs	
27100	>10	AA404231		EST - RC_AA404231	
11329	>10	AA216589	Hs.28462	ESTs	
4402	>10	U41518	Hs.74602	AQUAPORIN-CHIP	
11050	>10	AA142919	Hs.5558	ESTs	
22844	>10	R98947		EST - RC_R98947	
31581	>10	N71371	Hs.39938	ESTs	
7253	>10	AA074407	Hs.139119	ESTs	
20423	>10	N49308	Hs.104938	ESTs	
39264	>10	AA621750		EST - RC_AA621750	
36415	>10	AA426598	Hs.24897	Homo sapiens chromosome 21q22.1 anonymous mRNA sequence	
16575	>10	AA031948	Hs.57548	ESTs	
37505	>10	AA455659	Hs.103233	ESTs	
28264	>10	AA521080	Hs.46765	ESTs	
23886	>10	T95325	Hs.16545	ESTs	
11781	>10	AA256485	Hs.33413	ESTs	
25603	>10	AA114250	Hs.48924	Homo sapiens mRNA for KIAA0512 protein complete cds	
9003	>10	C00808	Hs.107882	ESTs	
5632	>10	X15357		EST - X15357	
7680	>10	AA206946	Hs.8059	ESTs	
22783	>10	R95689	Hs.35437	ESTs	
20852	>10	N69540	Hs.17713	ESTs	
16795	>10	AA047896	Hs.49169	ESTs	
37558	>10	AA456975	Hs.75736	Apolipoprotein D	
35957	>10	AA412537	Hs.98149	EST	
42129	>10	T71561	Hs.84824	ESTs	
34585	>10	AA281002	Hs.40735	ESTs	
33690	>10	Z38607	Hs.62248	ESTs	
8904	>10	AF002256	Hs.66180	Homo sapiens killer cell receptor (KIR103) mRNA allele ASDJ complete cds	
2689	>10	M32373	Hs.1256	Arylsulfatase B	

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## FIGURE 7 (CONT.)

40909	>10	N63084	Hs.49608	ESTs	
22377	>10	R63090	Hs.28391	ESTs	
21208	>10	R07651	Hs.20023	EST	
27304	>10	AA421783	Hs.56808	Homo sapiens mRNA for zinc finger protein FPM315 complete cds	
3307	>10	M95809	Hs.89578	BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT	
25370	>10	AA057556	Hs.28478	ESTs	
41423	>10	R44717	Hs.22917	ESTs	
2570	>10	M27160	Hs.2053	Tyrosinase (oculocutaneous albinism IA)	
14557	>10	AA620965	Hs.108300	ESTs Highly similar to ADENYLOSUCCINATE SYNTHETASE MUSCLE ISOZYME [Mus musculus]	
7023	>10	Z78291	EST - Z78291		
31051	>10	N62696	Hs.48607	EST	
39200	>10	AA621246	Hs.112956	EST	
24712	>10	Z39652	Hs.27457	ESTs	
23296	>10	T52497	Hs.9444	ESTs Moderately similar to III: ALU CLASS A WARNING ENTRY III: [H.sapiens]	
12826	>10	AA424806	Hs.134646	ESTs	
2199	>10	L49169	Hs.75678	Human GOS3 mRNA complete cds	
27226	>10	AA416787	Hs.43498	ESTs	
7135	>10	AA028976	Hs.8175	ESTs	
17102	>10	AA074955	EST - RC_AA074955		
38942	>10	AA609646	Hs.94970	Human mRNA for KIAA0306 gene partial cds	
29288	>10	H64973	Hs.38336	ESTs	
34336	>10	AA250843	Hs.54434	Interferon regulatory factor 5	
30816	>10	N63566	Hs.47681	ESTs	
16739	>10	AA045461	Hs.65093	ESTs	
42317	>10	T97599	Hs.113025	ESTs	
2228	>10	L77563	EST - L77563		
30862	>10	N55171	Hs.47927	ESTs	
35954	>10	AA412526	Hs.97951	ESTs	
38403	>10	AA426383	Hs.98467	ESTs	
36949	>10	AA441812	Hs.98959	ESTs	
41628	>10	R70212	Hs.79630	Immunoglobulin-associated alpha	
39175	>10	AA621076	Hs.111996	ESTs	
37657	>10	AA460147	EST - RC_AA460147		
36279	>10	AA424242	Hs.98397	ESTs Weakly similar to precursor of major fibrous sheath protein [M.musculus]	
6834	>10	Z18954	Hs.2960	S100 calcium-binding protein A5 (formerly S100D)	
40562	>10	N33212	Hs.107197	ESTs	
13770	>10	AA463272	Hs.22636	ESTs	
5101	>10	U79249	Hs.78362	Human clone 23839 mRNA sequence	
3355	>10	M99438	Hs.31305	Human transducin-like enhancer protein (TLE3) mRNA complete cds	
8476	>10	AA442119	Hs.29790	ESTs	

## FIGURE 7 (CONT.)

34231	>10	AA234527	Hs.75772	Glucocorticoid receptor
42046	>10	T59148	Hs.50966	Carbamoyl-phosphate synthetase 1 mitochondrial
23913	>10	T96123	Hs.17749	ESTs
37333	>10	AA452158	Hs.75122	TRANSFORMING PROTEIN RHOB
27946	>10	AA463434	Hs.42658	ESTs
34407	>10	AA255523	EST - RC_AA255523	ESTs
16542	>10	AA029428	Hs.61555	ESTs
6248	>10	X78712	Hs.98008	Glycerol kinase 2 (testis specific)
8227	>10	AA393666	Hs.75709	Mannose-6-phosphate receptor (calion dependent)
3507	>10	S78774	EST - S78774	ESTs
40907	>10	N68630	Hs.25717	ESTs
33340	>10	W79698	Hs.58550	ESTs
19079	>10	H06371	Hs.20945	ESTs
3992	>10	U19713	Hs.76364	Allograft inflammatory factor 1
36059	>10	AA417063	Hs.98189	ESTs
37634	>10	AA459662	Hs.99489	EST
41581	>10	R62313	Hs.126270	ESTs Weakly similar to RTP60 (R.norvegicus)
38734	>10	AA608792	Hs.112591	EST
37836	>10	AA470135	Hs.112236	ESTs
21303	>10	R11157	Hs.12610	ESTs
20125	>10	N22006	Hs.6202	ESTs
35516	>10	AA400795	Hs.97450	ESTs
26771	>10	AA284067	Hs.89287	EST
33558	>10	W50735	Hs.59332	EST
2830	>10	M57399	Hs.44	Pleiotrophin (heparin binding growth factor 8 neurite growth-promoting factor 1)
42625	>10	W88426	Hs.110128	ESTs
26152	>10	AA250845	Hs.87762	ESTs
31988	>10	N94581	Hs.55062	ESTs
17763	>10	AA148213	Hs.71873	ESTs Highly similar to 65 KD YES-ASSOCIATED PROTEIN (Gallus gallus)
21959	>10	R44949	Hs.22906	ESTs
10000	>10	N79674	Hs.7915	ESTs
30658	>10	N51105	Hs.111223	ESTs
17629	>10	AA131919	Hs.69009	ESTs
36260	>10	AA423970	Hs.98378	ESTs
285	>10	D16227	Hs.3618	Hippocaldin-like 1
26123	>10	AA243598	Hs.20887	ESTs
34535	>10	AA278391	Hs.104425	EST
29100	>10	H01428	Hs.92350	ESTs
24122	>10	W46947	Hs.4188	ESTs
19894	>10	H65942	Hs.36030	ESTs

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## FIGURE 7 (CONT.)

22987	>10	T16258	Hs.25420	ESTs	
5985	>10	X54728	Hs.34514	H. sapiens CHML mRNA	
42461	>10	W60008	Hs.89717	Human preprocarboxypeptidase A2 (proCPA2) mRNA complete cds	
5422	>10	X00588	Hs.77432	Epidermal growth factor receptor	
16603	>10	AA034366	Hs.144627	ESTs	
33389	>10	W81607	Hs.58663	EST	
6931	>10	Z46788	Hs.3232	H. sapiens mRNA for cyclin II	
19324	>10	H17618	Hs.28180	ESTs	
32166	>10	R41836	Hs.9657	ESTs	
39967	>10	H58415	Hs.102160	EST	
17958	>10	AA166917	Hs.72639	ESTs	
38569	>10	AA598437	Hs.29385	ESTs Highly similar to MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES ASSEMBLY PROTEIN RCA1 [Saccharomyces cerevisiae]	
1006	>10	HG2260-	Hs.29385	EST - HG2260-HT2349	
23552	>10	T79638	Hs.105618	ESTs	
38228	>10	AA468997	Hs.137530	ESTs	
1066	>10	HG2705-	EST - HG2705-HT2801		
23815	>10	T91283	EST - RC_T91283		
4699	>10	U57089	Human APEG-1 mRNA complete cds		
31306	>10	N66796	Hs.144212	ESTs	
12389	>10	AA399633	Hs.24872	ESTs	
34539	>10	AA279662	Hs.142462	ESTs Moderately similar to snRNP protein B [H. sapiens]	
20358	>10	N39584	Hs.17404	ESTs	
26070	>10	AA236868	Hs.87564	ESTs	
38210	>10	AA488659	Hs.105686	ESTs	
26025	>10	AA235874	Hs.88888	PUTATIVE DNA BINDING PROTEIN A20	
4978	>10	U71207	Hs.29279	Homo sapiens clone 24534 eyes absent homolog (Eab1) mRNA partial cds	
4935	>10	U68162	Hs.84171	THROMBOPOIETIN RECEPTOR PRECURSOR	
3501	>10	S78467	EST - S78467		
14281	>10	AA505136	Hs.12420	ESTs	
31859	>10	N90688	Hs.54643	EST	
41104	>10	R01398	EST - RC_R01398		
5293	>10	U89995	Hs.95206	Human DNA binding protein FKHL15 (FKHL15) mRNA complete cds	
3543	>10	S81957	EST - S81957		
27615	>10	AA443958	Hs.90960	ESTs	
7152	>10	AA036753	Hs.78494	Homo sapiens mRNA for KIAA0525 protein partial cds	
16197	>10	AA010328	Hs.39379	ESTs	
20176	>10	N24772	Hs.30213	Homo sapiens putative transmembrane protein (CLN5) mRNA complete cds	
33586	>10	W93015	Hs.73166	Treacher Collins syndrome susceptibility protein	
27265	>10	AA418392	Hs.46784	ESTs	
12453	>10	AA402000	Hs.20415	ESTs Weakly similar to GS3786 [H. sapiens]	

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## FIGURE 7 (CONT.)

36302	>10	AA424652	Hs.124985	ESTs	
23192	>10	T40448	Hs.8204	ESTs	
17423	>10	AA114071	Hs.26270	ESTs	
23464	>10	T67026	Hs.13019	ESTs	
42762	>10	Z41697	Hs.106296	ESTs	
32628	>10	T56470	Hs.119190	Chromogranin A (parathyroid secretory protein 1)	
12805	>10	AA424331	Hs.29640	ESTs	
25379	>10	AA058893	Hs.111841	Human adenyl cyclase-associated protein homolog CAP2 (CAP2) mRNA complete cds	
39318	>10	C20617	Hs.108945	Homo sapiens mRNA for KIAA0515 protein partial cds	
29699	>10	H97938	Hs.75772	Glucocorticoid receptor	
17907	>10	AA160530	Hs.72447	ESTs	
35819	>10	AA411011	Hs.8038	ESTs	
36838	>10	AA435163	Hs.95851	Homo sapiens Pig12 (PIG12) mRNA complete cds	
29611	>10	H94043	Hs.41949	ESTs	
19650	>10	H46167	Hs.31542	ESTs	
33221	>10	W70305	Hs.64859	ESTs	
18840	>10	F10265	Hs.13287	ESTs	
2580	>10	M27533	EST - M27533	ESTs	
7274	>10	AA082171	Hs.8261	ESTs	
19524	>10	H29566	Hs.83466	Homo sapiens clone 23579 mRNA sequence	
40571	>10	N33558	Hs.103102	ESTs Weakly similar to WWP2 [H.sapiens]	
29894	>10	N64191	Hs.46584	ESTs	
22201	>10	R54416	Hs.140932	ESTs	
26718	>10	AA282583	Hs.88617	ESTs	
32493	>10	T16497	Hs.65339	EST	
37179	>10	AA448004	Hs.99150	ESTs	
17980	>10	AA169173	Hs.72754	ESTs	
21934	>10	R44449	Hs.48778	ESTs	
36792	>10	AA435848	EST - RC_AA435848	ESTs	
34056	>10	AA194851	Hs.110575	ESTs	
39102	>10	AA620674	Hs.112882	EST	
26283	>10	AA253217	Hs.41271	ESTs	
23989	>10	T98529	Hs.18398	ESTs	
32456	>10	T15829	Hs.65264	ESTs	
15440	>10	W27301	Hs.111652	ESTs Moderately similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA [Thermomonospora curvata]	
19004	>10	H03299	Hs.30390	EST	
27839	>10	AA456309	Hs.58831	ESTs	
18848	>10	F10338	Hs.106309	ESTs Moderately similar to FOG [M.musculus]	
13112	>10	AA435896	Hs.18397	ESTs	

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## FIGURE 7 (CONT.)

1850	>10	L17325	Hs.278	Human pre-TNK cell associated protein (1D12A2) mRNA complete cds
9101	>10	C17938	Hs.25536	ESTs
2807	>10	M55210	Hs.87428	Laminin gamma 1 (formerly LAMB2)
3383	>10	S57153	Hs.91797	Retinoblastoma-binding protein 1 (alternative products)
23142	>10	T26444	Hs.101248	ESTs
5367	>10	U95019	Hs.30941	Myasthenic syndrome antigen B (human fetal brain mRNA 3477 nt)
32205	>10	R44234	Hs.75169	ESTs
26515	>10	AA262972	Hs.87298	ESTs
15332	>10	W24127	Hs.16003	ESTs Weakly similar to keratin 8 type II cytoskeletal embryonic (M.musculus)
34193	>10	AA232251	Hs.128630	ESTs
6392	>10	X85753	Hs.25283	CELL DIVISION PROTEIN KINASE 8
33784	>10	Z40689	Hs.65973	ESTs
33474	>10	W87484	Hs.50429	ESTs
34964	>10	AA344854	Hs.96837	ESTs
14584	>10	AA621414	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
22640	>10	R83684	Hs.33416	EST
4339	>10	U38372	EST - U38372	
37557	>10	AA456966	Hs.41548	Human MHC Class I region proline rich protein mRNA complete cds
4937	>10	U68385	Hs.117313	Human Meis1-related protein 2 (MRG2) mRNA partial cds
30795	>10	N53043	Hs.47606	ESTs
30966	>10	N59432	Hs.48382	EST
33991	>10	AA181935	Hs.104059	EST
2265	>10	M11591	EST - M11591	
24315	>10	W84413	Hs.23017	ESTs
38752	>10	AA608852	Hs.112603	EST
5119	>10	U79271	Hs.7571	Human clones 23920 and 23921 mRNA sequence
15037	>10	U44798	Hs.93502	Human U1-snRNP binding protein homolog mRNA complete cds
37045	>10	AA446000	Hs.99043	ESTs
37627	>10	AA459392	Hs.105042	ESTs
21935	>10	R44477	Hs.22646	ESTs
18669	>10	F03889	Hs.27278	ESTs Highly similar to PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A [Bos taurus Sus scrofa]
22737	>10	R92512	EST - RC_R92512_s	
30727	>10	N51987	Hs.47390	EST
16086	>10	AA001879	Hs.59890	EST
23293	>10	T52201	Hs.9410	ESTs
5294	>10	U90065	Hs.79351	Human two P-domain K+ channel TWIK-1 mRNA complete cds
17769	>10	AA148923	Hs.93675	ESTs
25549	>10	AA101056	EST - RC_AA101056	
84	>10	AF001359	EST - AF001359_f	
4856	>10	U65093	Hs.82071	Human msg1-related gene 1 (mrg1) mRNA complete cds

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## FIGURE 7 (CONT.)

7697	>10	AA214730	Hs.107256	ESTs	
36296	>10	AA424535	Hs.98416	ESTs	
17490	>10	AA125781	Hs.57489	ESTs	
36976	>10	AA442779	Hs.96983	ESTs	
10425	>10	AA010619	Hs.16446	ESTs	
41196	>10	R11654	Hs.20526	ESTs	
42285	>10	T94409	EST - RC_T94409		
33185	>10	W69435	Hs.58009	EST	
13974	>10	AA479299	Hs.21107	ESTs	
19868	>10	H61560	EST - RC_H61560		
1378	>10	HG831-	EST - HG831-HT831		
621	>10	D63813	Hs.26886	Human mRNA for rod photoreceptor protein complete cds	
5346	>10	U92459	Hs.86204	Human metabotropic glutamate receptor 8 mRNA complete cds	
6029	>10	X66533	Hs.77890	GUANYLATE CYCLASE SOLUBLE BETA-1 CHAIN	
22196	>10	R53972	Hs.26026	ESTs	
24609	>10	Z38900	Hs.26615	ESTs	
37196	>10	AA448226	EST - RC_AA448226		
26151	>10	AA250836	ESTs		
5938	>10	X62535	Hs.74044	Diacylglycerol kinase alpha (80kD)	
16373	>10	AA019603	Hs.60992	ESTs	
26356	>10	AA609080	Hs.41585	ESTs	
20070	>10	H98854	Hs.20423	ESTs	
17717	>10	AA136541	Hs.71647	EST	
20069	>10	H98768	Hs.13121	ESTs	
40985	>10	N74604	Hs.124694	ESTs	
10194	>10	R63545	Hs.11553	ESTs Weakly similar to putative type III alcohol dehydrogenase [D.melanogaster]	
40200	>10	H87229	Hs.82963	Gonadotroph-releasing hormone (leutinizing-releasing hormone)	
34983	>10	AA347417	Hs.96869	EST	
23543	>10	T79203	Hs.14480	ESTs	
12770	>10	AA421778	Hs.8861	ESTs	
25085	>10	AA017518	Hs.115241	Homo sapiens G protein beta 5 subunit mRNA complete cds	
37746	>10	AA463627	Hs.99598	ESTs	
2370	>10	M16505	Hs.79876	STERYL-SULFATASE PRECURSOR	
31244	>10	N66062	Hs.49112	EST	
37116	>10	N75507	Hs.59628	ESTs Weakly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP17 [Rattus norvegicus]	
28306	>10	AA598959	Hs.59163	ESTs	
2220	>10	L76887	Hs.83070	Homo sapiens Grb14 mRNA complete cds	
12404	>10	AA400292	Hs.23786	ESTs	
41050	>10	N92882	Hs.109494	ESTs Weakly similar to putative progesterone binding protein [H.sapiens]	
2407	>10	M18737	Hs.90708	GRANZYME A PRECURSOR	

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## FIGURE 7 (CONT.)

23462	>10	T66948	Hs.12992	ESTs	
18614	>10	F02418	Hs.107614	ESTs	
40553	>10	N32060	Hs.104010	Homo sapiens CAG-1st 7 mRNA complete cds	
27826	>10	AA455949	Hs.61232	ESTs	
207	>10	D12763	Hs.66	Suppression of tumorigenicity 2	
41064	>10	N93608	Hs.102923	EST	
10845	>10	AA084405	Hs.106313	ESTs Weakly similar to P24 protein [M.musculus]	
21813	10	R42039	Hs.23084	ESTs	
18463	10	AA233151	Hs.81796	ESTs	
17507	10	AA126419	Hs.74876	ESTs	
23957	10	T97487	Hs.18070	ESTs	
13317	10	AA448212	Hs.38095	ESTs	
29550	10	H90133	Hs.41352	ESTs	
39068	10	AA620411	Hs.141503	Small Inducible cytokine A5 (RANTES)	
26620	10	AA280413	Hs.89843	Spleen focus forming virus (SFFV) proviral integration oncogene spl1	
37675	10	AA460377	Hs.99816	ESTs	
31437	10	N68821	Hs.49573	ESTs	
32857	10	T68867	Hs.76889	ESTs	
34952	10	AA342828	Hs.73734	PLATELET GLYCOPROTEIN V PRECURSOR	
26475	10	AA262264	Hs.87640	ESTs	
41827	10	T15445	Hs.59491	H.sapiens mRNA for F25B3.3 kinase like protein from C.elegans	
20073	10	H98985	Hs.11911	ESTs	
42336	10	T99713	Hs.139933	ESTs	
26412	10	AA258224	Hs.86646	ESTs	
21352	10	R15880	Hs.21745	ESTs	
22583	10	R79239	Hs.29855	EST	
34020	10	AA191543	Hs.144302	EST	
25913	10	AA161106	EST - RC_AA161106		
82	10	AF000959	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds	
37531	10	AA456140	Hs.99235	ESTs	
13314	10	AA448169	Hs.6728	ESTs	
31430	10	N68610	EST - RC_N68610		
30570	10	N49587	Hs.46633	EST	
7302	10	AA085688	Hs.103668	EST	
27732	10	AA452167	Hs.55778	ESTs	
22533	10	R73468	Hs.140996	ESTs	
31079	10	N62969	Hs.48682	EST	
35470	10	AA400393	Hs.97803	EST Weakly similar to precursor polypeptide [H.sapiens]	
37102	10	AA446869	Hs.119316	ESTs	
203	10	D12620	Hs.108242	CYTOCHROME P450 IVF3	

## FIGURE 7 (CONT.)

11427	10	AA233277	Hs.74947	ESTs	
24159	10	W57862	Hs.21289	ESTs	
17870	10	AA157772	Hs.72185	ESTs	
5302	10	U90543	Hs.79041	Human butyrophilin (BTF1) mRNA complete cds	
27256	10	AA417998	Hs.62781	ESTs	
2219	10	L76670	Hs.109610	Homo sapiens nkat7 mRNA complete cds	
30858	10	N55081	Hs.47815	EST	
8870	10	AB002367	Hs.21355	Human mRNA for KIAA0369 gene complete cds	
40870	10	N67262	Hs.358	Zinc finger protein 135 (clone pHZ-17)	
11811	10	AA258130	Hs.11530	ESTs	
33254	10	W72633	Hs.58187	ESTs	
17162	10	AA079094	EST - RC_AA079094		
24392	10	W88568	Hs.58589	Homo sapiens glycogenin-2 gamma (glycogenin-2) mRNA complete cds	
27456	10	AA430539	Hs.57760	ESTs	
25419	10	AA069386	EST - RC_AA069386		
7100	10	AA012885	Hs.60548	ESTs	
31586	10	N71571	Hs.50050	ESTs	
29995	10	N26401	Hs.43802	EST	
31973	10	N93875	Hs.55015	EST	
36159	10	AA419279	Hs.82813	Colony-stimulating factor 1 (M-CSF)	
12419	10	AA400888	Hs.7159	ESTs	
27076	10	AA401630	Hs.62592	ESTs	
4219	10	U32324	Hs.64310	Human Interleukin-11 receptor alpha chain mRNA complete cds	
28251	10	AA504512	Hs.76852	ESTs Weakly similar to ZK792.1 [C.elegans]	
27991	10	AA465650	Hs.87306	ESTs	
37702	10	AA461119	Hs.95539	ESTs	
25251	10	AA040792	Hs.54421	Bradykinin receptor B2	
27054	10	AA401253	Hs.87677	ESTs	
37592	10	AA458668	Hs.95898	ESTs	
39619	9	F10640	Hs.12354	ESTs	
31053	9	N62724	Hs.48614	EST	
33338	9	W79524	Hs.58585	ESTs	
23368	9	T59005	Hs.10476	EST	
8240	9	AA397841	Hs.106879	ESTs	
21778	9	R41389	Hs.26159	EST	
31168	9	N63965	Hs.48903	ESTs	
3440	9	S72370	Hs.89890	Pyruvate carboxylase	
25930	9	AA164928	EST - RC_AA164928		
29971	9	N25657	Hs.93692	EST	
39771	9	H17463	Hs.101735	ESTs	

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## FIGURE 7 (CONT.)

21481	9	R26141	Hs.24032	ESTs Highly similar to transmembrane receptor [M.musculus]
10887	9	AA101632	Hs.22971	ESTs
31431	9	N68666	Hs.76788	ESTs
30756	9	N52398	Hs.39252	ESTs
35829	9	AA411438	Hs.74635	Dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex 2-oxo-glutarate complex branched chain keto acid dehydrog
24540	9	Z38435	Hs.19235	ESTs
37500	9	AA455474	Hs.100530	ESTs
19007	9	H03358	EST - RC_H03358	
42650	9	W92272	Hs.25601	Homo sapiens zinc-finger helicase (hZFh) mRNA complete cds
16705	9	AA043675	Hs.62633	EST
40275	9	H94647	Hs.102329	ESTs
24372	9	W87423	Hs.35598	ESTs
9011	9	C01394	Hs.106823	Homo sapiens clone 24818 mRNA sequence
40780	9	N59568	Hs.108107	ESTs
17177	9	AA079331	EST - RC_AA079331	
20878	9	N70305	Hs.34492	ESTs
38140	9	AA486273	Hs.100472	ESTs
3490	9	S77763	Hs.75643	Homo sapiens NF-E2 protein (NF-E2) mRNA complete cds
38112	9	AA620724	Hs.112890	ESTs
27347	9	AA424940	Hs.43590	ESTs
14747	9	D60364	Hs.34882	ESTs
23599	9	T82307	EST - RC_T82307	
23979	9	T98262	EST - RC_T98262	
27759	9	AA453472	Hs.95111	ESTs
36691	9	AA432381	Hs.97357	ESTs Moderately similar to NITRIC OXIDE SYNTHASE INDUCIBLE [H.sapiens]
26782	9	AA284181	Hs.69310	ESTs
26818	9	AA285145	Hs.50446	ESTs
22334	9	R61290	Hs.25870	ESTs
29892	9	N22595	Hs.42829	ESTs
22945	9	T10134	Hs.9877	Homo sapiens mRNA for KIAA0688 protein complete cds
30618	9	N50556	Hs.93996	ESTs Highly similar to mosaic protein LR11 [H.sapiens]
29715	9	H98700	Hs.60887	ESTs
37560	9	AA457023	EST - RC_AA457023	
23264	9	T50062	Hs.9092	EST
31001	9	N62200	Hs.47566	ESTs
17841	9	AA156109	Hs.66180	ESTs
3478	9	S76992	Hs.104005	Vav 2 oncogene
11605	9	AA243139	Hs.4863	ESTs
19032	9	H04822	Hs.30494	EST
29933	9	N24182	Hs.93677	ESTs

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## FIGURE 7 (CONT.)

26622	9	AA280431	Hs.88756	ESTs	
4289	9	U35376	Hs.37138	Human repressor transcriptional factor (ZNF85) mRNA complete cds	
42034	9	T56281	Hs.110440	Human metallothionein (MT)-F gene	
30447	9	N47439	Hs.44603	ESTs	
25238	9	AA039568	Hs.44603	ESTs	
20238	9	N30077	Hs.14855	EST - RC_AA039568	
30232	9	N34500	Hs.44800	ESTs	
17017	9	AA069920	Hs.10839	EST - RC_AA069920	
11845	9	AA259064	Hs.10839	ESTs Weakly similar to unknown [S.cerevisiae]	
30229	9	N34457	Hs.47442	EST - RC_N34457	
30737	9	N52137	Hs.47442	EST	
30555	9	N49259	Hs.93956	EST - RC_N49259	
981	9	HG2139	Hs.93956	EST - HG2139-HT2208_f	
30498	9	N48325	Hs.93956	EST	
40434	9	N21461	Hs.95594	EST - RC_N21461	
36788	9	AA435824	Hs.95594	Homo sapiens BAC clone RG113D17 from 7p14-p15	
28991	9	F04652	Hs.66195	ESTs	
25942	9	AA234187	Hs.87267	ESTs	
30466	9	N47951	Hs.57485	ESTs	
19317	9	H17476	Hs.11615	ESTs Weakly similar to dual specificity phosphatase [H.sapiens]	
13859	8	AA470066	Hs.24309	ESTs Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE MEDIUM CHAIN [Rattus norvegicus]	
23445	8	T65992	Hs.11722	EST	
24448	8	W93273	Hs.9270	ESTs Weakly similar to isopentenyl-diphosphate Delta-isomerase [H.sapiens]	
7583	8	AA167824	Hs.63559	ESTs Highly similar to PROTEIN CDC27HS [Homo sapiens]	
22718	8	R94840	Hs.35372	ESTs Weakly similar to IIII ALU CLASS B WARNING ENTRY IIII [H.sapiens]	
16439	8	AA024835	Hs.47584	Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA complete cds	
42395	8	W42733	Hs.109870	ESTs	
19991	8	H90887	Hs.18357	ESTs	
23690	8	T87648	Hs.18357	EST - RC_T87648	
7111	8	AA018804	Hs.125175	ESTs Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]	
6400	8	X86163	Hs.54421	Bradykinin receptor B2	
42474	8	W63747	Hs.109918	H.sapiens TTF mRNA for small G protein	
11425	8	AA233257	Hs.25511	Homo sapiens mRNA for Hic-5 partial cds	
27039	8	AA400277	Hs.46849	ESTs	
32206	8	R44386	Hs.91703	ESTs	
15310	8	W19098	Hs.7921	ESTs	
36601	8	AA431337	Hs.98017	ESTs	
463	8	D38462	Hs.50482	EST - D38462	
31674	8	N74357	Hs.50482	ESTs	
31182	8	N64339	Hs.48956	EST	

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## FIGURE 7 (CONT.)

13499	8	AA453458	Hs.7301	ESTs	
37514	8	AA455914	Hs.1019	Parathyroid hormone receptor 1	
5998	8	X65644	Hs.75063	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2	
962	8	HG180-		EST - HG180-HT180	
40790	8	N62328	Hs.3786	Glutamate receptor, metabotropic 3	
25700	8	AA131512	Hs.103820	EST	
36880	8	AA436706	Hs.98895	ESTs	
2809	8	M55267	Hs.41846	EV12A PROTEIN PRECURSOR TROPIC VIRAL INTEGRATION SITE 2A PROTEIN)	
5620	8	X14885	Hs.2025	Transforming growth factor beta 3	
16643	8	AA039325	Hs.47200	ESTs	
32051	8	R01450	Hs.91061	ESTs	
33550	8	W90517	Hs.50120	ESTs	
6177	8	X75535	Hs.118884	33 KD HOUSEKEEPING PROTEIN	
33000	8	W45531	Hs.94642	ESTs	
20066	8	H98701	Hs.4985	ESTs	
4590	8	U50534	Hs.30649	Human infant brain mRNA clone 13cDNA73	
37199	8	AA448257	Hs.97127	ESTs	
24601	8	Z38844	Hs.25803	ESTs	
33589	8	W93074	Hs.59342	ESTs	
37389	8	AA453466	Hs.99330	ESTs	
5801	8	X55448	Hs.3118	H. sapiens mRNA for 2.19 gene	
28748	8	D25912	Hs.74832	ESTs	
40070	8	H72592	Hs.77554	ESTs	
40367	8	H98857	Hs.75520	Human mRNA for KIAA0041 gene partial cds	
33609	8	W93585	Hs.59476	ESTs	
24502	8	Z38214	Hs.26946	ESTs	
11129	8	AA156873	Hs.15970	ESTs	
7144	8	AA033659	Hs.95154	ESTs	
28584	8	C21221	Hs.68619	ESTs Highly similar to METALLOTHIONEIN-1A [Equus caballus]	
22165	8	R52822	Hs.22003	ESTs	
31987	8	N94551	Hs.55060	ESTs	
32470	8	T15956	Hs.65289	EST	
38642	8	AA599152	Hs.91379	PTB-ASSOCIATED SPLICING FACTOR	
40438	8	N21684	Hs.80500	Human mRNA for KIAA0061 gene partial cds	
34471	8	AA258843	Hs.111376	ESTs	
41571	8	R61005	Hs.115170	Homo sapiens mRNA for GaiT4 protein	
31417	8	N68435	Hs.49516	ESTs	
23851	8	T97318	Hs.18037	ESTs	
7832	8	AA249260	Hs.28545	ESTs	
27928	8	AA461093	Hs.26799	ESTs Moderately similar to zinc finger protein [R. norvegicus]	

## FIGURE 7 (CONT.)

2017	8	L34219	Hs.1933	Cellular retinaldehyde-binding protein
25530	8	AA098834	Hs.83428	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)
20556	8	N55189	Hs.34081	ESTs
27036	8	AA400135	Hs.142935	ESTs
22651	7	R85266	Hs.33487	ESTs
33663	7	W95805	Hs.59736	EST
19374	7	H19472	Hs.31653	EST
10275	7	R79356	Hs.19280	ESTs Weakly similar to PROTEIN Q300 [Mus musculus]
39471	7	D60265	Hs.107894	ESTs
25100	7	AA019426	Hs.103343	EST
8828	7	AB002316	Hs.65746	Human mRNA for KIAA0318 gene partial cds
17132	7	AA075674		EST - RC_AA075674
15915	7	Y09858	Hs.82577	Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34) hypothetical prote
8216	7	AA393089	Hs.86723	ESTs
22512	7	R71489	Hs.29196	EST
19097	7	H08171	Hs.30842	ESTs
25048	7	AA011041	Hs.130843	ESTs
35353	7	AA398862	Hs.97699	ESTs
31278	7	N66399	Hs.49193	EST
23149	7	T26893	Hs.7569	EST
11860	7	AA262763	Hs.22057	ESTs
17547	7	AA127595	Hs.71016	ESTs
32854	7	W32094	Hs.55501	ESTs
36822	7	AA435978	Hs.98852	EST
35530	7	AA400893	Hs.41717	Human 3'5' cyclic nucleotide phosphodiesterase (HSPDE1A3A) mRNA complete cds
3869	7	U14417	Hs.106185	Human Rat guanine nucleotide dissociation stimulator mRNA partial cds
9368	7	H09246	Hs.100739	ESTs
15154	7	U79527	Hs.111075	Human orphan G-protein coupled receptor Dez isoform a mRNA complete cds
21178	7	R06607	Hs.19748	EST
33081	7	W57731	Hs.56213	ESTs
13848	7	AA465664	Hs.21323	ESTs
18659	7	F03220	Hs.13258	ESTs
1979	7	L29339	Hs.1964	Solute carrier family 5 (sodium/glucose cotransporter) member 1
22609	7	R80945	Hs.29978	ESTs
2418	7	M19507	Hs.1817	Myeloperoxidase
28853	7	D80051	Hs.124418	ESTs
26764	7	AA283926	Hs.51501	ESTs
6544	7	X95677		EST - X95677
33524	7	W89188	Hs.59096	ESTs
18374	7	AA226877	Hs.67624	ESTs

## FIGURE 7 (CONT.)

10108	7	R25069	Hs.23790	ESTs	
26178	7	AA251153	Hs.27910	Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA complete cds	
36428	7	AA427605	Hs.98551	Human cardiac myosin binding protein-C (MyBP-C) gene complete cds	
29808	7	N21032	Hs.42931	EST	
24837	7	Z41188	Hs.27997	ESTs	
24909	7	Z98492	Hs.27250	ESTs	
26333	7	AA256075	Hs.82280	Homo sapiens regulator of G protein signaling 10 mRNA complete cds	
11507	7	AA235465	Hs.29161	ESTs	
40387	7	H99460	Hs.10873	ESTs	
16112	7	AA004377	Hs.91813	Human butyrophilin (BTF2) mRNA complete cds	
25413	7	AA065096	EST - RC_AA065096		
13232	7	AA443844	Hs.20887	ESTs	
27236	7	AA417037	Hs.67805	ESTs	
21684	7	R38944	Hs.129672	ESTs	
9294	7	D82712	Hs.15301	ESTs Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-ori7 protein [C.elegans]	
16886	7	AA057119	Hs.5091	Homo sapiens torsinB (DQ1) mRNA partial cds	
20083	7	H99879	Hs.28029	ESTs Highly similar to EPIDERMAL GROWTH FACTOR PRECURSOR [Mus musculus]	
30651	7	N51029	Hs.38672	ESTs	
22362	7	R62447	Hs.22123	ESTs	
21561	7	R33245	Hs.23076	ESTs	
21636	7	R37501	Hs.23600	ESTs	
21223	7	R08175	Hs.110130	Homo sapiens chromosome 19 cosmid F22329	
32218	7	R45654	Hs.1339	Collagen type IV alpha 2	
13405	7	AA450118	Hs.25722	ESTs Weakly similar to KRUPPEL-RELATED ZINC FINGER PROTEIN 1 [Homo sapiens]	
30827	7	N50740	Hs.47111	ESTs	
30117	7	N30824	Hs.44227	ESTs Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	
31344	7	N67238	EST - RC_N67238		
38119	7	AA485714	Hs.105669	ESTs	
33297	7	W73781	Hs.105715	ESTs	
5892	7	Z30426	Hs.82401	CD59 antigen (early T cell activation antigen)	
9923	7	N44998	Hs.24550	ESTs	
27942	7	AA463237	Hs.13021	ESTs	
34845	7	AA293420	Hs.95464	ESTs Moderately similar to transcription enhancer factor TEF1 [H.sapiens]	
29829	7	N21460	Hs.43005	ESTs	
15059	7	U53831	Hs.85280	Human interferon regulatory factor 7 (humirf7) mRNA complete cds	
40441	7	N22053	Hs.112083	ESTs	
25095	7	AA018937	Hs.109558	ESTs	
2941	7	N62840	Hs.82542	Acylglycyl hydrolase (neutrophil)	
1945	7	L25878	Hs.89649	Epoxide hydrolase 1 microsomal (xenobiotic)	
42648	7	W92150	Hs.79310	Human GAP SH3 binding protein mRNA complete cds	

## FIGURE 7 (CONT.)

19582	7	H40696	Hs.33780	ESTs	
29801	7	N20939	Hs.38759	ESTs	
15417	7	W26982	Hs.39330	ESTs	
39877	7	H38627	Hs.107696	ESTs	
23967	7	T97910	Hs.18184	EST	
20041	7	H97012	Hs.11050	ESTs Weakly similar to L8004.7 gene product [S.cerevisiae]	
18314	7	AA214510	Hs.86618	ESTs	
22452	7	R67370	Hs.28758	ESTs	
30496	7	N48294	Hs.46850	EST	
26830	7	AA287057	Hs.48820	ESTs	
33432	7	W66075	Hs.38715	ESTs	
31394	7	N67990	Hs.49421	ESTs	
7053	6	Z84721	Hs.75792	Hemoglobin alpha 1	
33518	6	W88996	Hs.59134	EST	
5355	6	U94320	Hs.123021	Human Y5 receptor mRNA complete cds	
41311	6	R38516	Hs.124255	EST	
12545	6	AA406320	Hs.24702	ESTs	
23843	6	T92561	Hs.110422	ESTs	
21667	6	R38475	Hs.21408	ESTs	
17472	6	AA121704	Hs.69494	ESTs	
25648	6	AA126673	Hs.110341	ESTs	
32710	6	T87324	Hs.91021	EST	
3450	6	S73840	Hs.931	H.sapiens mRNA for fast 2a myosin heavy chain (3' end)	
979	6	HG2090-		EST - HG2090-HT2152	
8151	6	AA348686		EST - AA348686	
35380	6	AA399522	Hs.97671	ESTs Weakly similar to T04A8.9 [C.elegans]	
23798	6	T91047	Hs.126785	ESTs	
940	6	HG1496-		EST - HG1496-HT1496	
35896	6	AA412106	Hs.97349	ESTs	
16350	6	AA019034	Hs.94000	ESTs	
27547	6	AA436613	Hs.72157	ESTs	
22528	6	R73036	Hs.29323	EST	
25815	6	AA149889	Hs.96200	ESTs Weakly similar to A-kinase anchor protein 95 AKAP95 [R.norvegicus]	
8473	6	AA437346	Hs.2967	SHB adaptor protein (a Src homology 2 protein)	
35742	6	AA406058	Hs.97999	EST	
36538	6	AA430002	Hs.112044	ESTs	
17831	6	AA152323	Hs.71947	ESTs	
25072	6	AA015799	Hs.33792	ESTs	
15632	6	W56102	Hs.71218	ESTs	
20442	6	N50827	Hs.25275	ESTs	



## FIGURE 7 (CONT.)

28357	6	AA609120	Hs.56185	ESTs Weakly similar to The KIAA0147 gene product is related to adenylyl cyclase. [H.sapiens]
25022	6	AA007591	Hs.110227	ESTs
29334	6	H68158	Hs.28310	ESTs
28148	6	AA488875	Hs.6433	Homo sapiens clone 24523 mRNA sequence
30744	6	N52195	Hs.105365	H.sapiens mRNA for arginine methyltransferase
27577	6	AA442090	Hs.119295	ESTs
33472	6	W87469	Hs.58992	ESTs
25687	6	AA130867	Hs.100119	ESTs
10549	6	AA027317	Hs.19136	ESTs Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]
32836	6	W23631	Hs.55426	ESTs
17025	6	AA070160	EST - RC_AA070160	
22939	6	T10070	Hs.4217	Homo sapiens mRNA for KIAA0567 protein partial cds
15803	6	X52332	Hs.104115	Human Kox1 gene for zinc finger protein
34618	6	AA282143	Hs.58094	H.sapiens mRNA for melanoma growth regulatory protein MIA
11074	6	AA148983	Hs.29068	ESTs
12212	6	AA297746	Hs.22654	ESTs
16102	6	AA002150	Hs.59872	ESTs
31340	6	N67197	Hs.50125	EST
19459	6	H24317	Hs.6526	ESTs
17533	6	AA127098	Hs.71057	EST
22017	6	R46597	Hs.22703	ESTs
23687	6	T87519	Hs.16075	ESTs Weakly similar to no similarities to reported gene products [H.sapiens]
30298	6	N36130	Hs.44792	EST Weakly similar to hypothetical protein [H.sapiens]
28973	6	F04014	Hs.65996	ESTs
17042	6	AA070397	EST - RC_AA070397	
20817	6	N68628	Hs.37630	ESTs
18430	6	AA232138	Hs.118898	ESTs
28493	6	C14820	Hs.67186	EST
30497	6	N48302	Hs.46852	EST
32502	6	T16896	Hs.65373	ESTs
41324	6	R38804	Hs.13434	Homo sapiens clone 24418 mRNA sequence
18418	6	AA228096	Hs.60480	ESTs
23622	6	T84046	Hs.15345	ESTs
15342	6	W25781	Hs.8136	Homo sapiens clone 23698 mRNA sequence
15246	6	W01094	Hs.84628	ESTs
2247	6	M10321	Hs.110802	VON WILLEBRAND FACTOR PRECURSOR
31906	6	N92643	Hs.35986	Homo sapiens CASK mRNA complete cds
9062	6	C06238	Hs.95665	Homo sapiens clone 24700 unknown mRNA partial cds
38640	6	AA599142	Hs.112509	EST
42622	6	W87801	Hs.108209	ESTs

## FIGURE 7 (CONT.)

27908	6	AA460571	Hs.54837	ESTs	
7293	6	AA085354	EST - AA085354		
27322	6	AA424325	Hs.40496	ESTs	
5774	6	X54199	Hs.82285	Phosphoribosylglycinamide formyltransferase phosphoribosylglycinamide synthetase phosphoribosylamidimidazole synthetase	
33469	6	W87454	Hs.58987	ESTs Highly similar to homogenisate 12-dioxygenase [H.sapiens]	
40329	6	H97488	Hs.108802	Human N-ethylmaleimide-sensitive factor mRNA partial cds	
26539	6	AA278848	Hs.88522	ESTs	
23579	6	T81098	Hs.124085	ESTs	
22435	6	R66706	Hs.28706	ESTs	
19958	6	H80842	Hs.37445	ESTs	
18607	6	F02345	Hs.21197	ESTs	
18991	6	H02554	Hs.30323	ESTs	
7810	6	AA248169	Hs.106709	ESTs Highly similar to LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR [Rattus norvegicus]	
30810	6	N53419	Hs.47648	ESTs	
17996	6	AA169606	Hs.72815	ESTs	
26245	6	AA252357	Hs.87794	ESTs	
13348	8	AA449287	Hs.17914	ESTs Weakly similar to HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT [M.musculus]	
15034	6	U43701	Hs.75403	60S RIBOSOMAL PROTEIN L23A	
33802	6	Z41058	Hs.79248	ESTs	
33394	6	W84432	Hs.56670	ESTs	
31170	6	N64017	Hs.48911	ESTs	
40828	6	N64144	Hs.102749	EST	
1789	6	L13258	Hs.936	Solute carrier family 17 (sodium phosphate) member 2	
17740	5	AA142922	Hs.9817	Homo sapiens Arg/Abi-interacting protein ArgBP2a (ArgBP2a) mRNA complete cds	
9509	5	H58970	Hs.49883	ESTs	
15540	5	W30895	Hs.7535	ESTs	
27827	5	AA455976	Hs.42355	ESTs	
30697	5	N51585	Hs.47049	ESTs	
40299	5	H95787	Hs.103745	ESTs	
16827	5	AA038779	Hs.61826	Homo sapiens clone 23928 mRNA sequence	
20659	5	N62915	Hs.57672	ESTs Weakly similar to weakly similar to myosin heavy chain [C.elegans]	
31009	5	N62272	Hs.48502	ESTs	
14877	5	T65508	Hs.14623	Homo sapiens mRNA for KIAA0625 protein partial cds	
31102	5	N63178	Hs.48728	ESTs	
22830	5	R98421	EST - RC_R98421	ESTs	
25248	5	AA040507	Hs.92924	ESTs	
32145	5	R38910	Hs.66170	Homo sapiens clone 24503 mRNA sequence	
27970	5	AA464626	Hs.10247	Activated leucocyte cell adhesion molecule	
34509	5	AA262974	Hs.111394	ESTs	
29522	5	H88338	Hs.90250	ESTs	

## FIGURE 7 (CONT.)

32159	5	R40974	Hs.124270	ESTs	
35492	5	AA400514	Hs.97505	ESTs	
37630	5	AA459649	Hs.99485	ESTs	
27103	5	AA404282	Hs.63481	ESTs	Weakly similar to kynurenine/alpha-aminoadipate aminotransferase [R.norvegicus]
17209	5	AA082933		EST - RC_AA082933	
589	5	D50930	Hs.5084	Human mRNA for KIAA0140 gene complete cds	
17489	5	AA122394	Hs.70811	ESTs	
6293	5	X80878	Hs.95262	Human R kappa B mRNA complete cds	
5067	5	U77845	Hs.21254	Human hTRIP (hTRIP) mRNA complete cds	
23060	5	T23513	Hs.7147	ESTs	
28902	5	D80990	Hs.45247	ESTs	
32328	5	R76401	Hs.92262	ESTs	
33218	5	W70259	Hs.48523	ESTs	
28751	5	D45455	Hs.65524	ESTs	
21400	5	R19360	Hs.14651	ESTs	
15557	5	W36290	Hs.9115	ESTs	
12631	5	AA412293	Hs.21258	ESTs	
32282	5	R62579	Hs.62264	ESTs	
10416	5	AA009809	Hs.37589	ESTs	
40308	5	H96306	Hs.32980	Human mRNA for BST-1 complete cds	
11599	5	AA242829	Hs.7508	ESTs	
33220	5	W70279	Hs.94811	ESTs	Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]
23100	5	T23867	Hs.7316	ESTs	
15333	5	W24154	Hs.6166	ESTs	
8331	5	AA412556		EST - AA412556	
9010	5	C01360	Hs.67384	Homo sapiens clone 23904 mRNA sequence	
4660	5	U53225	Hs.75283	Sorting nexin 1	
25213	5	AA035444	Hs.100543	Homo sapiens clone 24505 mRNA sequence	
25242	5	AA039933	Hs.30941	Myasthenic syndrome antigen B [human fetal brain mRNA 3477 nt]	
28708	5	D20538	Hs.90165	EST	
7435	5	AA096412	Hs.26236	ESTs	
25538	5	AA099580	Hs.101442	ESTs	Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]
271	5	D14823		EST - D14823	
5490	5	X04571	Hs.2230	Epidermal growth factor	
18812	5	F10040	Hs.13251	ESTs	
23393	5	T62918	Hs.11110	ESTs	Weakly similar to ZINC FINGER PROTEIN 42 [H.sapiens]
23446	5	T66282	Hs.12907	ESTs	
35204	5	AA398155	Hs.97600	ESTs	
31369	5	N67598	Hs.136395	ESTs	
5244	5	U85992	Hs.87197	Human clone IMAGE:35527 unknown protein mRNA partial cds	

## FIGURE 7 (CONT.)

20835	5	N69215	Hs.37456	ESTs	
16502	5	AA027059	Hs.61425	EST	
23691	5	T87693	Hs.16414	ESTs	
31842	5	N90168	Hs.54593	EST	
7845	5	AA249611	EST - AA249611		
29297	5	H65459	Hs.38323	ESTs	
7953	5	AA284403	Hs.74750	Homo sapiens mRNA for KIAA0554 protein partial cds	
36412	5	AA426464	Hs.98466	ESTs	
19357	5	H18929	EST - RC_H18929		
16299	5	AA016258	EST - RC_AA016258		
25312	5	AA047078	ESTs Weakly similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! [H.sapiens]		
27617	5	AA446114	Hs.55409	ESTs	
42432	5	W46403	Hs.107293	ESTs	
38432	5	AA496983	Hs.78672	Laminin alpha 4	
32215	5	R45175	Hs.117183	ESTs	
15214	5	U93553	Hs.91310	Human alpha1-fetoprotein transcription factor (hFTF) mRNA complete cds	
15141	5	U78788	Hs.90957	Human TNF receptor associated factor 6 (TRAF6) mRNA complete cds	
20052	5	H97922	Hs.5376	Human LAR-interacting protein 1a mRNA complete cds	
7551	5	AA156838	Hs.107941	ESTs	
26451	5	AA259058	Hs.43616	ESTs	
42355	5	W20404	Hs.55405	ESTs	
39480	5	D60419	Hs.81915	STATHMIN	
17369	5	AA101833	Hs.69293	EST	
14993	5	U22172	Hs.73046	Human DNA damage repair and recombination protein RAD52 pseudogene mRNA partial cds	
23400	5	T63336	Hs.105095	ESTs	
21153	5	R05315	EST - RC_R05315		
14282	5	AA505141	Hs.11923	ESTs	
21104	5	R01081	EST - RC_R01081		
32825	5	W20364	Hs.55412	ESTs	
35018	5	AA349591	EST - RC_AA349591		
25104	5	AA019598	Hs.103351	ESTs	
19235	5	H12725	Hs.31181	ESTs	
34979	5	AA347209	Hs.7841	Human mRNA for KIAA0324 gene partial cds	
21501	5	R26855	Hs.24120	ESTs	
18331	5	AA218543	Hs.10881	Homo sapiens mRNA for KIAA0541 protein partial cds	
37529	5	AA456112	Hs.99410	ESTs	
15532	5	W28944	Hs.5296	ESTs Highly similar to PUTATIVE 2-HYDROXYACID DEHYDROGENASE IN BISC-CSPA INTERGENIC REGION [Escherichia coli]	
11858	5	AA262308	Hs.106385	ESTs	
29450	5	H80865	Hs.111026	Phosphatidylinositol glycan class F	
37294	5	AA450127	Hs.110571	ESTs Highly similar to MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118 [Mus musculus]	

## FIGURE 7 (CONT.)

35170	5	AA397830	Hs.98347	ESTs Weakly similar to rtvp-1 [H.sapiens]
23201	5	T40652	Hs.9279	ESTs
27012	5	AA398913	Hs.45231	ESTs
28767	5	D45608	Hs.83792	Surfactant pulmonary-associated protein D
17777	5	AA149634	Hs.62788	ESTs Weakly similar to hypothetical L1 protein [H.sapiens]
20588	5	N58009	Hs.36218	ESTs
20356	5	N39453	Hs.27371	ESTs
23375	5	T59670	Hs.10615	EST
17030	5	AA070188	EST - RC_AA070188	
30752	5	N52340	Hs.118084	EST
25808	5	AA149226	Hs.95821	Human osteoclast stimulating factor mRNA complete cds
31345	5	N67268	Hs.50139	ESTs
30784	5	N52857	Hs.47558	ESTs
13707	5	AA460281	Hs.14697	ESTs
29199	5	H25761	Hs.57082	EST
39003	4	AA609920	Hs.112785	EST
41529	4	R54458	Hs.2699	Glypican 1
3151	4	M83652	Hs.53155	Properdin P factor complement
33134	4	W61264	Hs.57829	ESTs
29196	4	H24456	Hs.85053	Homo sapiens clone 24440 mRNA sequence
12863	4	AA425782	Hs.27973	ESTs
11949	4	AA279827	Hs.125035	ESTs
31925	4	N92924	Hs.125032	ESTs
35258	4	AA398428	Hs.97628	ESTs
39838	4	H27216	Hs.107635	ESTs
30796	4	N53045	Hs.91146	ESTs Moderately similar to [H.sapiens]
19464	4	H24458	Hs.32085	EST
42486	4	W68410	Hs.108857	Calbindin 2 (29kD calretinin)
34274	4	AA236352	Hs.110821	ESTs
37648	4	AA459917	Hs.99506	EST
3169	4	M85085	Hs.693	Cleavage stimulation factor 3' pre-RNA subunit 2 64kD
10326	4	R96417	Hs.107795	ESTs
15063	4	U56814	Hs.88646	Homo sapiens DNase gamma mRNA complete cds
23571	4	T80628	Hs.108169	ESTs
14377	4	AA596583	Hs.15299	ESTs Weakly similar to HSM-2 [H.sapiens]
22255	4	R56239	Hs.6666	ESTs
36820	4	AA435958	Hs.98849	ESTs Weakly similar to bithoraxoid [D.melanogaster]
35063	4	AA358015	Hs.96998	EST
12376	4	AA399271	Hs.19510	ESTs
31406	4	N68163	Hs.49455	EST

## FIGURE 7 (CONT.)

27430	4	AA429028	Hs.42678	ESTs	Moderately similar to IIII ALU SUBFAMILY SB WARNING ENTRY [III] [H.sapiens]
30362	4	N40170	Hs.45046	ESTs	
30599	4	N50039	Hs.47004	ESTs	
27894	4	AA460319	Hs.48469	ESTs	
31844	4	N90218	Hs.54607	ESTs	
24935	4	AFX-			AFX-HUMGAPDH/M33197_M
40906	4	N68829	Hs.131510	ESTs	
35220	4	AA398246	Hs.97594	ESTs	
10024	4	N94832	Hs.121699	ESTs	
4238	4	U33053	Hs.2499	Human lipid-activated protein kinase PRK1 mRNA complete cds	
26358	4	AA256396	Hs.88156	EST	
24716	4	Z39734	Hs.22550	ESTs	
19243	4	H13539	Hs.31222	ESTs	
41844	4	T15633	Hs.100227	EST	
39774	4	H17948	Hs.106311	Homo sapiens DGS-A mRNA 3' end	
20111	4	N21380	Hs.25497	H.sapiens mRNA for ROX protein	
24008	4	T99337	Hs.18624	ESTs	
8316	4	AA410529	Hs.30732	ESTs	
35072	4	AA358738		EST - RC_AA358738	
39794	4	H21819	Hs.14896	Homo sapiens clone 24590 mRNA sequence	
1517	4	J04501	Hs.772	Glycogen synthase 1 (muscle)	
9164	4	D38081	Hs.89887	Thromboxane A2 receptor	
35027	4	AA349996	Hs.96937	ESTs	
35185	4	AA398015	Hs.97590	Unfilled	
26570	4	AA279425	Hs.86428	ESTs Weakly similar to hypothetical L1 protein [H.sapiens]	
19759	4	H54352	Hs.36873	ESTs	
34310	4	AA243416	Hs.75470	Homo sapiens mRNA expressed in osteoblast complete cds	
39961	4	H57317	Hs.108161	ESTs	
23249	4	T47919	Hs.8749	ESTs	
19119	4	H09077	Hs.30895	EST	
14158	4	AA490182	Hs.118598	ESTs	
22866	4	R99938	Hs.36189	EST	
16935	4	AA059392	Hs.66791	ESTs	
41950	4	T33137	Hs.7967	ESTs	
20404	4	N48694	Hs.30881	Homo sapiens lipin-alpha2 mRNA complete cds	
18406	4	AA227962	Hs.112075	ESTs Weakly similar to reverse transcriptase [M.musculus]	
16560	4	AA031308	Hs.24341	ESTs	
26098	4	AA242831	Hs.87608	ESTs	
34360	4	AA251547	Hs.104358	EST	
16830	4	AA054222	Hs.40400	ESTs	

## FIGURE 7 (CONT.)

32686	4	T69284	Hs.2314	Mannose-binding lectin soluble (opsonic defect)
32912	4	W38051	EST - RC_W38051	
16230	4	AA011549	Hs.47884	ESTs
29696	4	H97909	Hs.42344	ESTs
8232	4	AA397529	EST - AA397529	
25584	4	AA112320	Hs.16704	ESTs
30878	4	N56882	Hs.46761	EST
40579	4	N34524	Hs.102516	ESTs
8026	4	AA301842	Hs.105189	ESTs Weakly similar to reverse transcriptase homolog [H.sapiens]
3094	4	M77481	Hs.72879	Human antigen (MAGE-1) gene complete cds
17480	4	AA121974	EST - RC_AA121974	
15766	4	W95777	Hs.90804	ESTs
34865	4	AA299903	Hs.111498	EST
29779	4	N20290	Hs.42836	ESTs
6547	4	X95808	Hs.9568	Human mRNA for KIAA0385 gene complete cds
24479	4	W96222	Hs.34192	ESTs
16135	4	AA004805	Hs.63668	Human Toll-like receptor 2 (TLR2) mRNA complete cds
11098	4	AA151243	Hs.38163	ESTs
14388	4	AA599742	Hs.21600	ESTs
36078	4	AA417275	Hs.98214	ESTs
23440	4	T65566	Hs.12859	ESTs
20863	4	N69989	Hs.19167	ESTs
20347	4	N39117	Hs.12250	ESTs
7795	4	AA247455	Hs.15220	ESTs
10729	4	AA054087	Hs.18858	ESTs
12734	4	AA419200	Hs.5737	ESTs
24446	4	W93119	Hs.19512	ESTs
30734	4	N52083	Hs.47418	EST
20641	4	N62353	Hs.109585	ESTs
21183	4	R06769	Hs.19795	ESTs
18138	4	AA192757	Hs.131687	ESTs
35310	4	AA398662	Hs.97302	ESTs
39497	4	D80154	Hs.56340	ESTs
29866	4	N22343	Hs.43145	ESTs
8707	4	AA479995	Hs.76982	Human sapiens mRNA for KIAA0583 protein partial cds
18472	4	AA233299	Hs.72158	ESTs
24720	4	Z39754	Hs.23236	ESTs
40825	4	N63923	Hs.102746	ESTs
15375	4	W26395	Hs.56876	ESTs
32869	4	W35211	Hs.54801	ESTs

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## FIGURE 7 (CONT.)

4641	4	U52426	Hs.74597	Homo sapiens GOK (STIM1) mRNA complete cds
11786	4	AA256616	Hs.31707	ESTs
21571	4	R33841	Hs.24709	ESTs Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]
1600	4	K03474		EST - K03474
21103	4	R01058	Hs.14603	ESTs
22993	4	T16358	Hs.106443	ESTs
38666	4	AA599661	Hs.103849	ESTs
27148	4	AA406231	Hs.100113	Human mRNA for KIAA0381 gene partial cds
28080	4	D20261	Hs.80067	ESTs
36397	4	AA426372	Hs.109804	Human mRNA for histone H1x complete cds
26915	4	AA330634		EST - RC_AA330634
6912	4	Z35278	Hs.2536	H.sapiens PEBP2aC1 acute myeloid leukaemia mRNA
31825	4	N89848	Hs.54543	ESTs
10763	4	AA057620	Hs.30807	ESTs
17007	4	AA069696	Hs.67317	ESTs
33439	4	W88445	Hs.56844	ESTs
27657	4	AA447612	Hs.60435	ESTs
26288	4	AA253393	Hs.87734	ESTs
8235	4	AA397616	Hs.107245	ESTs Moderately similar to potassium channel protein Raw3 [R.norvegicus]
12114	4	AA287097	Hs.25114	ESTs
879	4	D88155	Hs.97196	Human steroidogenic factor 1 mRNA complete cds
30793	4	N52979	Hs.51919	Plasminogen-like protein
13522	4	AA454115	Hs.6000	ESTs
20819	4	N68730	Hs.12160	ESTs
20019	4	H94266	Hs.9451	ESTs
32396	4	R95778	Hs.93008	EST
38162	4	AA487165	Hs.105705	EST
8487	4	AA442669		EST - AA442669
18444	4	AA232646	Hs.68061	ESTs
16183	4	AA010070	Hs.60339	EST
33047	4	W49755	Hs.89359	ESTs Moderately similar to type Ia hair keratin a3 [H.sapiens]
14797	4	S82769	Hs.104133	GABAA receptor gamma 3 subunit [human fetal brain mRNA Partial 1536 nt]
26107	3	AA243172	Hs.87619	ESTs
24421	3	W92001	Hs.120969	ESTs
27665	3	AA447759	Hs.134724	ESTs
19154	3	H10047	Hs.22515	ESTs
10933	3	AA121360	Hs.27567	ESTs Weakly similar to similar to alpha-13-mannosyl-glycoprotein beta-1 2-N-acetylglucosaminyltransferase [C.elegans]
7254	3	AA074897		EST - AA074897
18684	3	F04262	Hs.22137	ESTs
40997	3	N77904	Hs.44380	ESTs

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## FIGURE 7 (CONT.)

14971	3	U10493	Hs.438	Human Mox1 protein (MOX1) mRNA complete cds
11217	3	AA180487	Hs.62440	ESTs
16782	3	AA047265	Hs.82582	Homo sapiens mRNA for osteoblast specific cysteine-rich protein complete cds
21477	3	R26094	Hs.23531	ESTs
21382	3	R16896	Hs.89815	PROTEIN KINASE C THETA TYPE
19508	3	H28966	Hs.89815	EST - RC, H28966
30301	3	N36174	Hs.2507	SHYDROXYTRYPTAMINE 2B RECEPTOR
21553	3	R33005	Hs.23153	ESTs Weakly similar to ETX1 (alternatively spliced) [H.sapiens]
6102	3	X70340	Hs.2023	Transforming growth factor alpha
23502	3	T70580	Hs.13759	ESTs
8333	3	AA412620	Hs.4248	ESTs
30500	3	N48329	Hs.30490	ESTs Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]
21431	3	R22057	Hs.23338	ESTs
35920	3	AA412290	Hs.98124	ESTs
12065	3	AA283907	Hs.110480	Homo sapiens clone 23837 mRNA sequence
19156	3	H10068	Hs.25924	Homo sapiens clone 24466 mRNA sequence
24844	3	Z41301	Hs.23539	ESTs
33178	3	W68846	Hs.141719	EST
2052	3	L36818	Hs.75339	Inositol polyphosphate phosphatase-like protein 1 (51C protein)
15327	3	W23474	Hs.23352	ESTs
18874	3	F10585	Hs.12345	ESTs
9039	3	C02049	Hs.106291	ESTs
37470	3	AA454935	Hs.99566	ESTs
19167	3	H10641	Hs.22928	ESTs
34888	3	AA303078	Hs.94479	Human GT334 protein (GT334) gene mRNA complete cds
30591	3	N49952	Hs.138717	ESTs
26997	3	AA398488	Hs.93090	ESTs
18647	3	F03004	Hs.27109	ESTs
17867	3	AA157291	Hs.72163	ESTs
15280	3	W07019	Hs.35088	ESTs
20465	3	N51599	Hs.14633	ESTs
11047	3	AA142849	Hs.22860	ESTs
19451	3	H23747	Hs.31697	ESTs
41621	3	R69233	Hs.101504	ESTs
2822	3	M55621	Hs.117946	N-acetylglucosaminyltransferase I
26675	3	D20188	Hs.74876	ESTs
13928	3	AA478441	Hs.11590	ESTs
29473	3	H83694	Hs.40478	ESTs
25829	3	AA151621	Hs.110984	ESTs
28532	3	C20680	Hs.68513	EST

## FIGURE 7 (CONT.)

32376	3	R91391	Hs.64391	ESTs	
12064	3	AA283848	Hs.11367	ESTs Weakly similar to KIAA0009 [H.sapiens]	
15547	3	W32012	Hs.29353	ESTs	
40284	3	H95073	Hs.108734	ESTs Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]	
22861	3	R99595	Hs.36152	ESTs	
15525	3	W28763	Hs.16349	Homo sapiens KIAA0431 mRNA partial cds	
17968	3	AA187496	Hs.72695	EST	
3836	3	U12707	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	
4528	3	U48251	Hs.75871	Homo sapiens protein kinase C-binding protein RACK7 mRNA partial cds	
29784	3	N20468	Hs.42849	ESTs Weakly similar to line-1 protein ORF2 [H.sapiens]	
7892	3	AA262100		EST - AA262100	
15279	3	W05746	Hs.133302	ESTs	
42064	3	T63364	Hs.9225	ESTs Highly similar to FIBRINOGEN-LIKE PROTEIN A PRECURSOR [Parasitichopus parvihnensis]	
17943	3	AA165117	Hs.20509	ESTs	
4596	3	U50743	Hs.19520	Sodium/potassium ATPase gamma subunit	
16421	3	AA022541	Hs.61146	ESTs	
4914	3	U67611		EST - U67611	
38171	3	AA487301	Hs.105713	EST	
20168	3	N24106	Hs.2799	Cartilage linking protein 1	
18791	3	F09892	Hs.12575	ESTs	
24281	3	W79773	Hs.16511	ESTs	
13996	3	AA480907	Hs.15769	ESTs	
20583	3	N57797	Hs.34421	ESTs	
37181	3	AA448158	Hs.99152	EST	
21450	3	R23146	Hs.23468	ESTs	
19634	3	H44866	Hs.31597	ESTs	
10163	3	RS4534	Hs.7698	Homo sapiens clone 23938 mRNA sequence	
7059	3	Z96810		EST - Z96810	
25762	3	AA136068	Hs.91797	Retinoblastoma-binding protein 1 (alternative products)	
27426	3	AA428900	Hs.92897	ESTs	
29023	3	F09302		EST - RC_F09302	
10989	3	AA132366	Hs.8023	Homo sapiens mRNA for SPOP	
6587	3	X97748		EST - X97748	
8722	3	AA481309	Hs.30204	ESTs	
21476	3	R26065	Hs.23523	ESTs	
14096	3	AA487558	Hs.8135	ESTs	
35392	3	AA399562	Hs.97568	ESTs	
28608	3	C21509	Hs.112774	ESTs	
13350	3	AA449297	Hs.8944	ESTs Weakly similar to type 1 procollagen C-proteinase enhancer protein precursor [H.sapiens]	
41202	3	R12808	Hs.113619	ESTs	

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## FIGURE 7 (CONT.)

15612	3	V51955	Hs.73372	ESTs	
33930	3	AA169539	Hs.95870	ESTs	
34215	3	AA233855	Hs.104252	UTROPHIN	
19208	3	H11734	Hs.110454	ESTs Weakly similar to coded for by C. elegans cDNA cm10a3 [C.elegans]	
24047	3	W15386	Hs.26750	ESTs	
14852	3	T52099	Hs.100383	ESTs Highly similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [Rattus norvegicus]	
27815	3	AA455370	Hs.59729	ESTs	
22610	3	R81173	Hs.11482	ESTs Highly similar to F11 antigen [H.sapiens]	
37510	3	AA453896	Hs.2699	ESTs Glypican 1	
37825	3	AA470073	Hs.104836	ESTs	
13321	3	AA448238	Hs.16714	ESTs	
25999	3	AA235375	Hs.87421	EST	
9738	3	M13150	Hs.99900	MAS1 oncogene	
16248	3	AA013125	Hs.40871	ESTs	
27592	3	AA442858	Hs.61979	ESTs Moderately similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [H.sapiens]	
16546	3	AA029452	Hs.95162	ESTs	
16981	3	AA064859		EST - RC_AA064859	
22128	3	R51021	Hs.23161	EST - RC_AA064859	
23312	3	T54617		EST - RC_AA064859	
18783	3	F09741	Hs.124205	ESTs	
10308	3	R86920	Hs.127585	ESTs	
22518	3	R71892	Hs.25998	ESTs Highly similar to 40S RIBOSOMAL PROTEIN S27A [Homo sapiens Cavia porcellus]	
8255	3	AA400226	Hs.25024	ESTs Weakly similar to estrogen-responsive finger protein efp [H.sapiens]	
16361	3	AA019218	Hs.40550	ESTs Moderately similar to proto-cadherin 3 [R.norvegicus]	
5453	3	X02910	Hs.2037	Tumor necrosis factor	
22509	3	R71393	Hs.29180	ESTs	
20065	3	H98657	Hs.27291	ESTs	
31091	3	N63076	Hs.138746	EST	
39050	3	AA610112	Hs.124849	ESTs	
2493	3	M22919	Hs.77385	MYOSIN LIGHT CHAIN ALKALI SMOOTH-MUSCLE ISOFORM	
30159	3	N32823	Hs.44069	ESTs	
28913	3	F01560	Hs.22583	ESTs Highly similar to co-repressor protein [M.musculus]	
12257	3	AA350030	Hs.4221	ESTs	
359	3	D26350	Hs.75119	Human mRNA for type 2 Inositol 145-itsphosphate receptor complete cds	
23587	3	T81358	Hs.14906	ESTs	
14323	3	AA598575	Hs.12651	ESTs	
27231	3	AA416936	Hs.7491	ESTs	
34914	3	AA338729	Hs.133096	ESTs	
21233	3	R08359	Hs.19308	ESTs	
23660	3	T86475	Hs.16193	ESTs	

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## FIGURE 7 (CONT.)

14236	3	AA496891	Hs.5011	ESTs Weakly similar to The ha1237 gene product is related to S.pombe rad21 gene product. [H.sapiens]
17617	3	AA131394	Hs.44672	ESTs Weakly similar to The KIAA0147 gene product is related to adenylyl cyclase. [H.sapiens]
24594	3	Z38804	Hs.22555	ESTs Highly similar to OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR [Bos taurus]
7426	3	AA095885	Hs.111818	Homo sapiens heat shock factor binding protein 1 HSBP1 mRNA complete cds
34871	3	AA300151	Hs.125146	ESTs
17962	3	AA167051	Hs.83525	Human brain mRNA homologous to 3'UTR of human CD24 gene partial sequence
24337	3	W66007	Hs.8876	ESTs
22589	3	R79580	Hs.29874	ESTs
24554	3	Z38522	Hs.27082	EST
22348	3	R61750	Hs.6136	ESTs
30217	3	N34288	Hs.44554	EST
10210	3	R67468	Hs.131828	ESTs
22156	3	R52145	Hs.25894	ESTs
16404	3	AA021284	Hs.60554	ESTs Moderately similar to sodium-calcium exchanger form 3 [R.norvegicus]
29310	3	H66642	Hs.88729	ESTs
15956	3	Z21217	Hs.77695	Human mRNA for KIAA0008 gene complete cds
9758	3	M26393	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
20917	3	N72295	Hs.16004	ESTs
4847	3	U64573	EST - U64573	
22984	3	T10362	Hs.57958	ESTs
9806	2	M79462	Hs.89633	Probable transcription factor PML (alternative products)
29807	2	N21031	Hs.42930	ESTs
39646	2	H02255	Hs.7268	Homo sapiens clone 23872 mRNA sequence
22733	2	R92181	Hs.34558	EST
23233	2	T41177	Hs.8410	Homo sapiens retinolic acid-inducible endogenous retroviral DNA
18549	2	F01360	Hs.6092	ESTs Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]
31892	2	N91968	Hs.39635	ESTs
18861	2	F10452	Hs.12254	ESTs
24553	2	Z38521	Hs.9428	ESTs
19289	2	H16568	Hs.23748	ESTs
14185	2	AA490911	Hs.22393	Homo sapiens dtp1 mRNA complete cds
30723	2	N51935	Hs.47374	EST
34031	2	AA192614	Hs.83577	Human LIM protein MLP mRNA complete cds
18434	2	AA232206	Hs.50743	ESTs
14647	2	D20378	Hs.30731	EST
41048	2	N92734	Hs.115985	ESTs
38157	2	AA486858	Hs.105702	EST
33299	2	W73790	Hs.73803	IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR
16616	2	AA035446	Hs.61783	ESTs
3276	2	M93718	Hs.76983	Nitric oxide synthase 3 (endothelial cell)

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## FIGURE 7 (CONT.)

33022	2	W46976	Hs.94667	EST	
31704	2	N75055	Hs.14632	ESTs	
38713	2	AA608577	Hs.112575	ESTs	
20396	2	N48293	Hs.12296	ESTs	
10310	2	R87373	Hs.75429	ESTs	
22388	2	R63695	Hs.1432	Protein kinase C substrate 80K-H	
15936	2	Z11737	Hs.2664	Flavin-containing monooxygenase 4	
23667	2	T86826	Hs.142528	ESTs	
30903	2	N57730	Hs.48058	EST	
20938	2	N73988	Hs.37477	ESTs Weakly similar to No definition line found [C.elegans]	
5935	2	X62466	Hs.108338	CDW52 antigen (CAMPATH-1 antigen)	
19304	2	H16976	Hs.7973	ESTs	
8804	2	AB000463	Hs.16227	Homo sapiens mRNA for SH3 binding protein complete cds done:RES4-23A	
41485	2	R49889	Hs.5260	ESTs Weakly similar to C06G8.3 [C.elegans]	
24685	2	Z39406	Hs.11797	ESTs Moderately similar to retinoid X receptor interacting protein [M.musculus]	
25403	2	AA063316	EST - RC_AA063316		
35773	2	AA409219	Hs.104747	ESTs	
27965	2	AA464267	Hs.24912	Homo sapiens bicuculal-D (BICD) mRNA complete cds	
16911	2	AA058659	Hs.60669	ESTs	
42315	2	T97353	EST - RC_T97353		
40632	2	N45221	EST - RC_N45221		
15722	2	W79046	Hs.15250	Homo sapiens DBI-related protein mRNA complete cds	
14842	2	T47519	EST - T47519		
36088	2	AA417344	Hs.98220	ESTs Moderately similar to located at OATL1 [H.sapiens]	
15527	2	W28798	Hs.63260	Phosphodiesterase 6A cGMP-specific rod alpha	
10302	2	R84933	Hs.133217	ESTs	
21243	2	R08773	Hs.20231	ESTs	
7759	2	AA234687	Hs.64147	ESTs Weakly similar to F59C6.4 [C.elegans]	
31672	2	N74336	Hs.91681	ESTs	
26799	2	AA284722	Hs.89121	ESTs	
25857	2	AA156504	Hs.95875	EST	
16695	2	AA043115	Hs.9452	ESTs Weakly similar to ORF YDL077c [S.cerevisiae]	
964	2	HG1804-	EST - HG1804-HT1829		
12439	2	AA401452	Hs.32080	ESTs	
19599	2	H41235	Hs.109968	ESTs	
24223	2	W70158	Hs.29696	ESTs	
21052	2	N93764	Hs.10175	ESTs Weakly similar to hypothetical protein [H.sapiens]	
17463	2	AA121338	EST - RC_AA121338		
28949	2	F03032	Hs.65826	ESTs Weakly similar to reverse transcriptase homolog [H.sapiens]	
34140	2	AA215637	Hs.104186	ESTs	

## FIGURE 7 (CONT.)

7465	2	AA120886	EST - AA120886
17376	2	AA102425	EST - RC_AA102425
5130	2	U79288	Hs.85053 Homo sapiens clone 24440 mRNA sequence
30041	2	N27628	Hs.132744 Homo sapiens clone 24525 mRNA sequence
19684	2	H48488	ESTs
8166	2	AA359093	EST - AA359093
19202	2	H11509	Hs.22482 ESTs
20439	2	N50785	Hs.13269 ESTs
10431	2	AA011310	Hs.3757 ESTs
29707	2	H98244	Hs.42519 ESTs
39868	2	H37909	Hs.107680 ESTs
8988	2	C00185	Hs.10444 ESTs
41350	2	R40442	Hs.75652 Glutathione S-transferase M5
13121	2	AA436156	Hs.110837 ESTs
15747	2	W88550	Hs.132188 ESTs
18674	2	F03989	Hs.18995 ESTs Weakly similar to KIAA0412 [H.sapiens]
914	2	HG1019	EST - HG1019-HT1019
23804	2	T91086	EST - RC_T91086
26556	2	AA279089	ESTs
8567	2	AA453381	ESTs
30457	2	N47686	Hs.64607 Human RACH1 (RACH1) mRNA complete cds
21975	2	R45441	Hs.23710 ESTs
17452	2	AA120766	Hs.70724 ESTs
31958	2	N93495	Hs.54960 ESTs
31495	2	N69850	Hs.49759 ESTs
32490	2	T16389	Hs.81248 Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA complete cds
39174	2	AA621067	Hs.112944 ESTs
21572	2	R34073	Hs.69740 Zinc finger protein 136 (clone pHZ-20)
15914	2	Y09846	Hs.81972 V-ski avian sarcoma viral oncogene homolog
12014	2	AA281769	Hs.7214 Human Hpast (HPAST) mRNA complete cds
39777	2	H18412	Hs.75253 Human clone ID 193225 NAD (H)-specific isocitrate dehydrogenase gamma subunit mRNA alternatively spliced partial cds
9484	2	H50178	Hs.108081 ESTs Highly similar to PROTEIN PHOSPHATASE PP2A 55 KD REGULATORY SUBUNIT NEURONAL ISOFORM [Oryctolagus cuniculus]
19147	2	H09751	Hs.117619 ESTs
36276	2	AA424179	Hs.124027 ESTs
16475	2	AA025903	Hs.57911 ESTs
21304	2	R11208	Hs.20755 ESTs
11199	2	AA176446	Hs.10024 ESTs
18093	2	AA187955	Hs.85564 ESTs
19190	2	H11274	Hs.31040 EST
15710	2	W76399	EST - W76399

## FIGURE 7 (CONT.)

18707	2	F04627	Hs.23540	ESTs	
6477	2	X91504	Hs.64904	Transcription factor COUP 2 (a.k.a. ARP1)	
20823	2	N68869	Hs.15119	ESTs	
16336	2	AA018601	Hs.75649	EXTRACELLULAR SIGNAL-REGULATED KINASE 3	
19680	2	H48457	Hs.35104	ESTs	
24833	2	Z41087	Hs.19066	ESTs	
24058	2	W23709	Hs.109047	ESTs	
26180	2	AA251230	Hs.112272	ESTs	
37177	2	AA447988	Hs.7765	ESTs	
14047	2	AA482597	Hs.26054	ESTs	
10770	2	AA058683	Hs.22552	ESTs	
41994	2	T47601	Hs.138805	ESTs	
19217	2	H12243	EST - RC_H12243		
36532	2	AA429889	Hs.68882	Acrosin	
23378	2	T60072	Hs.10688	ESTs	
1450	2	J03071	Hs.115352	Growth hormone 1	
8007	2	AA293072	Hs.97283	ESTs Moderately similar to IIII ALU CLASS B WARNING ENTRY IIII [H.sapiens]	
17266	2	AA084723	EST - RC_AA084723		
24819	2	Z40923	Hs.24812	ESTs	
6532	2	X95325	Hs.89491	DNA-BINDING PROTEIN A	
26850	2	AA287651	Hs.86641	ESTs	
34175	2	AA227523	Hs.108788	ESTs	
34620	2	AA282169	EST - RC_AA282169		
27085	2	AA402495	Hs.77978	ESTs	
20173	2	N24730	Hs.15420	ESTs	
17574	2	AA129060	EST - RC_AA129060		
22330	2	R60920	Hs.26419	Homo sapiens clone 24510 mRNA sequence	
30070	2	N29696	Hs.44076	EST	
20487	2	N52322	Hs.19978	ESTs	
724	2	D83703	Hs.30729	Peroxisomal biogenesis factor 6	
4132	2	U27655	Hs.82294	Human RGP3 mRNA complete cds	
8557	2	AA452705	Hs.23954	ESTs Weakly similar to D2045.9 [C.elegans]	
33659	2	W95628	Hs.59718	EST	
13375	2	AA449716	Hs.5723	ESTs	
30891	2	N57007	Hs.94074	EST	
13988	2	AA480045	Hs.7934	ESTs	
22306	2	R59906	Hs.100530	ESTs	
23167	2	T33164	Hs.12940	Homo sapiens germline mRNA sequence	
20873	2	N70134	Hs.31476	ESTs	
7231	2	AA059327	Hs.6580	Homo sapiens clone 23718 mRNA sequence	

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## FIGURE 7 (CONT.)

24582	2	Z38752	Hs.26330	ESTs	
11320	2	AA213667	Hs.22222	ESTs	
16388	2	AA020781	Hs.60647	ESTs	
24608	2	Z38888	Hs.25046	ESTs	
7809	2	AA248085	Hs.12469	Homo sapiens clone 23930 mRNA sequence	
13163	2	AA437225	Hs.22410	ESTs	
20549	2	N54991	Hs.37991	ESTs Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]	
1139	2	HG3227		EST - HG3227-HT3404	
35572	2	AA401489		EST - RC_AA401489	
6964	2	Z49105	Hs.137591	H.sapiens HD21 mRNA	
27704	2	AA449704	Hs.77637	Homo box A4	
33196	2	W69725	Hs.10711	ESTs	
30963	2	N59373	Hs.26812	ESTs	
13886	2	AA476937	Hs.24441	ESTs	
16164	2	AA007509	Hs.75395	Human mRNA for TPRD complete cds	
18083	2	AA181928	Hs.70954	Homo sapiens mRNA for hoxA7 protein	
20107	2	N21207	Hs.129942	ESTs Moderately similar to RETROVIRUS-RELATED POLYPROTEIN [Mus musculus]	
23004	2	T16556	Hs.6653	ESTs	
16238	2	AA011678	Hs.40470	ESTs	
18189	2	AA195042	Hs.65978	ESTs	
37587	2	AA457377		EST - RC_AA457377	
2174	2	L42611	Hs.111758	KERATIN TYPE II CYTOSKELETAL 6D	
38958	2	AA609707	Hs.112751	ESTs	
37919	2	AA478162	Hs.104965	ESTs	
28905	2	D81123	Hs.57475	ESTs	
33315	2	W74418	Hs.55410	ESTs	
7421	2	AA095600		EST - AA095600	
3745	2	U09117	Hs.80776	Human phospholipase c delta 1 mRNA complete cds	
19545	2	H37834	Hs.32699	ESTs	
21204	2	R07632	Hs.17949	ESTs	
8416	2	AA428531		EST - AA428531	
17569	2	AA128926		EST - RC_AA128926	
19372	2	H39195	Hs.22223	ESTs	
22760	2	R93714	Hs.33833	ESTs Highly similar to ALPHA-2-MACROGLOBULIN PRECURSOR [Homo sapiens]	
19354	2	H18829	Hs.121515	ESTs	
40618	2	N39565	Hs.106540	ESTs	
29913	2	N23708	Hs.43428	ESTs	
22571	2	R78665	Hs.136395	EST	
7598	2	AA174185	Hs.3354	Homo sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA complete cds	
25385	2	AA058099	Hs.109727	ESTs	

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## FIGURE 7 (CONT.)

14176	2	AA490620	Hs.11809	ESTs	
37400	2	AA453578	Hs.120994	ESTs	Weakly similar to T20D3.5 [C.elegans]
29487	2	H85120	Hs.80881	N-ACETYLACTOSAMINE SYNTHASE	
10197	2	R64199	Hs.50785	Homo sapiens vesicle trafficking protein sec22b mRNA complete cds	
322	2	D21241		EST - D21241_xp1	
22224	2	R55192	Hs.25689	ESTs	
19488	2	H27675	Hs.25604	ESTs	
10588	2	AA029703	Hs.36574	ESTs	
10872	2	AA099357	Hs.15780	ESTs	Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]
29987	2	N26172	Hs.43760	ESTs	
30799	2	N53143	Hs.64001	ESTs	
9638	2	L07592	Hs.106415	Human peroxisome proliferator activated receptor mRNA complete cds	
21069	2	N98461	Hs.17706	ESTs	
27195	2	AA411473	Hs.65311	EST - D79565	
9241	2	D79565	Hs.56896	ESTs	
9218	2	D61469	Hs.107287	ESTs	
22238	2	R55763	Hs.107287	ESTs	
7512	2	AA136369	Hs.2780	EST - AA136369	
17438	2	AA115508		Jun D proto-oncogene	
24932	2	AFEX		AFEX-HSAC07/X00351_M	
28911	2	F01325	Hs.3786	Glutamate receptor metabotropic 3	
10944	2	AA125969	Hs.34769	ESTs	Weakly similar to F35G12.9 [C.elegans]
42324	2	T98199	Hs.142702	ESTs	
37456	2	AA287665	Hs.8245	ESTs	
12743	2	AA421050	Hs.24545	ESTs	
21275	2	R10075	Hs.14890	ESTs	
13676	2	AA459389	Hs.26350	Homo sapiens mRNA for tyrosyl sulfotransferase-2	
13009	2	AA430474	Hs.16466	ESTs	
7403	2	AA094921	Hs.79788	ESTs	
11151	2	AA159961	Hs.25819	ESTs	
35669	2	AA404707	Hs.54865	ESTs	
17701	2	AA135941	Hs.71626	ESTs	
18713	2	F04688	Hs.21782	ESTs	
24144	2	W52312	Hs.30303	ESTs	Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]
30741	2	N52175	Hs.22222	ESTs	
23042	2	T23433	Hs.7105	ESTs	
18479	2	AA233483	Hs.87159	ESTs	
8314	2	AA410355	Hs.103081	ESTs	Highly similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens]
7990	2	AA291786	Hs.32822	ESTs	Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]
10388	2	AA005355		EST - RC_AA005355	

## FIGURE 7 (CONT.)

9407	2	H20086	EST - H20086	
42791	2	AFFX-	AFFX-HUMGAPDH/M33197_M	
26302	2	AA255470	ESTs	
30722	1	N51924	ESTs	
24965	1	AFFX-	AFFX-LysX-5	
38850	1	AA609262	EST - RC_AA609262	
13746	1	AA461300	ESTs	
6893	1	Z30643	Hs.30643	
31403	1	N68117	Hs.123123	H.sapiens mRNA for chloride channel (putative) 2139bp
17830	1	AA152312	ESTs	
10563	1	AA033874	Hs.72047	
20913	1	N72116	Hs.12035	
35607	1	AA402287	Hs.57435	Natural resistance-associated macrophage protein 2
9920	1	N44756	Hs.133475	ESTs Weakly similar to zinc finger protein [H.sapiens]
9468	1	H46074	Hs.141935	ESTs Weakly similar to transformation-related protein [H.sapiens]
29469	1	H82929	ESTs	
18121	1	AA191310	EST - RC_H82929	
14705	1	D59362	Protein phosphatase 2 (formerly 2A) regulatory subunit A (PR 65) beta isoform	
18692	1	F04444	EST - RC_D59362	
16543	1	AA029430	ESTs	
16359	1	AA019197	Hs.6217	
40818	1	N63772	Hs.61557	
35205	1	AA398161	Hs.40763	
7831	1	AA249175	Hs.144550	Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydro-
17794	1	AA150260	Hs.97602	
11347	1	AA24245	Hs.96334	ESTs Weakly similar to GOLIATH PROTEIN [Drosophila melanogaster]
17919	1	AA161125	Hs.72062	
22184	1	R53520	Hs.26612	
14827	1	T35288	Hs.72384	
28091	1	AA481788	Hs.102755	
28815	1	D59267	Hs.90421	
17813	1	AA151480	Hs.87593	
24655	1	Z39191	Hs.56782	
15611	1	W51743	Hs.91202	ESTs Weakly similar to Lph17p [S.cerevisiae]
39988	1	H62865	Hs.27262	
15700	1	W73859	Hs.35096	
22045	1	R48965	Hs.38132	
36770	1	AA435753	Hs.70061	Homo sapiens mesoderm-specific basic-helix-loop-helix protein (P-OD1) mRNA complete cds
9877	1	N31127	Hs.24796	
22467	1	R68284	EST - RC_AA435753	
	1		Hs.40098	
	1		Hs.28399	

## FIGURE 7 (CONT.)

32400	1	R97176	Hs.110783	ESTs	
10802	1	AA069425	Hs.20573	ESTs	
23033	1	T17353	Hs.108894	Homo sapiens clone 23918 mRNA sequence	
17593	1	AA129856	EST - RC_AA129856		
14867	1	T58588	Hs.100419	ESTs	
20266	1	N32118	Hs.107365	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]	
14447	1	AA609045	Hs.11759	ESTs	
37994	1	AA479919	EST - RC_AA479919		
12892	1	AA426521	Hs.18528	Homo sapiens mRNA for NA14 protein	
11970	1	AA280687	Hs.4069	ESTs	
19738	1	H53059	Hs.15548	ESTs	
14471	1	AA609346	Hs.20102	ESTs	
14855	1	T54762	Hs.9786	ESTs	
24725	1	Z39781	Hs.8004	Homo sapiens Duo mRNA complete cds	
5796	1	X55019	Hs.99975	Cholinergic receptor nicotinic delta polypeptide	
20259	1	N31598	Hs.12727	ESTs	
18441	1	AA232508	Hs.77480	ESTs	
18468	1	AA233177	Hs.87134	ESTs	
10164	1	R54743	Hs.19400	ESTs Weakly similar to MITOTIC MAD2 PROTEIN [S. cerevisiae]	
8630	1	AB002319	Hs.8663	Human mRNA for KIAA0321 gene partial cds	
15287	1	W07461	Hs.121559	ESTs Highly similar to DIPHTHINE SYNTHASE [Saccharomyces cerevisiae]	
16477	1	AA026031	Hs.61312	ESTs	
21969	1	R45334	Hs.21175	ESTs	
22340	1	R61522	Hs.26892	ESTs	
12884	1	AA426259	EST - RC_AA426259		
8682	1	AA477891	Hs.104476	ESTs	
22594	1	R79793	Hs.29900	ESTs	
19131	1	H09331	Hs.122791	ESTs	
17103	1	AA074997	EST - RC_AA074997		
35620	1	AA402493	Hs.10552	ESTs Highly similar to c-Jun leucine zipper interactive [M. musculus]	
35401	1	AA399593	Hs.97682	EST	
10901	1	AA112307	Hs.25224	ESTs	
19546	1	H37801	Hs.32706	ESTs	
15378	1	W26448	Hs.15071	ESTs Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]	
30292	1	N35978	Hs.82364	ESTs	
39087	1	AA620607	Hs.111591	ESTs	
37896	1	AA477463	Hs.77039	Ribosomal protein S28	
8636	1	AB002325	Hs.105917	Human mRNA for KIAA0327 protein complete cds	
16150	1	AA005428	Hs.60140	ESTs	
23955	1	T97467	Hs.18065	ESTs Weakly similar to alternatively spliced product using exon 13A [H. sapiens]	

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## FIGURE 7 (CONT.)

37812	1	AA469939	Hs.105323	ESTs	
14782	1	S72370	Hs.89890	Pyruvate carboxylase	
23540	1	T79178	Hs.14463	ESTs	
41552	1	R59352	Hs.101253	Human mRNA for KIAA0296 gene complete cds	
21836	1	R42569	Hs.22444	EST	
11467	1	AA234089	Hs.14593	ESTs	
18347	1	AA219230	Hs.86815	ESTs	
8215	1	AA389673	Hs.84344	ESTs	ESTs Weakly similar to No definition line found [C.elegans]
15505	1	W28366	Hs.7252	Homo sapiens clone 24800 mRNA sequence	
22764	1	R93802	Hs.33587	ESTs	
14966	1	U07620	Hs.89661	Human MAP kinase mRNA complete cds	
24213	1	W69184	Hs.23973	ESTs	
8165	1	AA358888	Hs.104135	Homo sapiens mRNA for DRIM protein	
32724	1	T90750	Hs.15230	ESTs	ESTs Weakly similar to F25H2.2 [C.elegans]
8212	1	AA386236	Hs.96757	Homo sapiens transcription factor SUPT3H (SUPT3H) mRNA complete cds	
9834	1	M92299	Hs.22554	Homo sapiens clone 23565 unknown mRNA partial cds	
7229	1	AA059213	Hs.91898	ESTs	
15649	1	W58725	Hs.75074	H.sapiens mRNA for MAP kinase activated protein kinase	
42306	1	T96538	Hs.45090	Human K+ channel beta 1a subunit mRNA alternatively spliced complete cds	
9159	1	D31483	Hs.90062	Homo sapiens clone 23565 unknown mRNA partial cds	
20040	1	H98712	Hs.125198	ESTs	
42218	1	T86444	Hs.110095	ESTs	
15526	1	W28790	Hs.8124	ESTs	
17790	1	AA150182	Hs.42262	ESTs	ESTs Weakly similar to HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III [C.elegans]
17595	1	AA129929	Hs.71166	EST	
31314	1	N65866	Hs.49278	EST	
9777	1	M57888	Hs.95946	GRANZYME H PRECURSOR	
15373	1	W26376	Hs.74563	THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR	
23547	1	T79448	Hs.14577	EST	
12076	1	AA284362	Hs.6448	ESTs	ESTs Weakly similar to No definition line found [C.elegans]
11956	1	AA279991	Hs.124691	ESTs	
15391	1	W26651	Hs.15961	ESTs	
9287	1	D82557	Hs.18104	ESTs	
16419	1	AA022466	Hs.61141	EST	
21713	1	R39930	Hs.21034	ESTs	
12905	1	AA427537	Hs.32419	ESTs	
30257	1	N34961	Hs.75873	H.sapiens mRNA for Zyxin	
28134	1	AA487622	Hs.64095	ESTs	
16380	1	AA019750	Hs.40797	ESTs	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]
10553	1	AA028904	Hs.33215	ESTs	

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## FIGURE 7 (CONT.)

18063	1	AA180054	Hs.73677	ESTs	
39820	1	H24085	Hs.25443	ESTs	
7374	1	AA093378	Hs.101810	ESTs	
13109	1	AA435838	Hs.7985	ESTs	
19378	1	H19673	Hs.31670	ESTs	
24325	1	W84733	Hs.3978	ESTs	
22318	1	R60224	Hs.7065	ESTs	
24249	1	W73069	Hs.12500	ESTs	
16514	1	AA027946	Hs.44608	ESTs	
21421	1	R21741	Hs.23258	EST	
8397	1	AA426178	Hs.71725	ESTs	Weakly similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! [H.sapiens]
8412	1	AA428090	Hs.26102	ESTs	
10072	1	R14782	Hs.31931	ESTs	
10349	1	AA001908	Hs.18160	ESTs	
14492	1	AA609635	Hs.27497	ESTs	
14930	1	T92512		EST - T92512	
15861	1	X81001	Hs.141503	Small Inducible cytokine A5 (RANTES)	
16706	1	AA043800	Hs.62645	ESTs	
16744	1	AA045643	Hs.62866	EST	
16950	1	AA062980	Hs.66960	ESTs	
17836	1	AA155779	Hs.29759	ESTs	Weakly similar to !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! [H.sapiens]
18634	1	F10207	Hs.13269	ESTs	
19178	1	H10992	Hs.100910	EST	
19767	1	H54720	Hs.36941	ESTs	
21341	1	R14959	Hs.21871	EST	Moderately similar to ninein [M.musculus]
21466	1	R24518	Hs.23674	EST	
21602	1	R36624	Hs.135137	ESTs	
21748	1	R40697	Hs.21290	EST	
21850	1	R43089		EST - RC_R43089	
21891	1	R43590	Hs.13290	ESTs	
21937	1	R44508	Hs.22653	ESTs	
22006	1	R46244	Hs.23110	ESTs	
22054	1	R49116	Hs.25067	EST	
22222	1	R55042	Hs.106645	ESTs	
22292	1	R59385	Hs.141053	Homo sapiens bestrophin (VMD2) mRNA alternatively spliced product complete cds	
22383	1	R63463	Hs.23282	ESTs	
22446	1	R67259	Hs.25968	EST	
23103	1	T29939	Hs.7344	ESTs	
23972	1	T94562	Hs.17338	EST	
24291	1	W80642	Hs.16951	ESTs	

## FIGURE 7 (CONT.)

24640	1	Z39086	Hs.21403	ESTs	
27519	1	AA435835	Hs.90895	ESTs	
32067	1	R06424	Hs.64896	ESTs	
32204	1	R44210	Hs.91440	EST	
32892	1	T79942	Hs.90930	ESTs	
33714	1	Z39430	Hs.65749	ESTs	
33733	1	Z39688	Hs.65792	ESTs	
33873	1	AFFX-	AFFX-DapX-3		
35434	1	AA400034	Hs.97769	EST	
35950	1	AA412498	Hs.104778	ESTs	
36483	1	AA428865	Hs.98563	EST	
36615	1	AA431469	Hs.98737	ESTs	
37329	1	AA452138	Hs.3781	Homo sapiens BAC clone RG118D07 from 7q31	
37700	1	AA461090	Hs.124826	EST	
38285	1	AA489840	Hs.105302	ESTs	
38887	1	AA609422	Hs.112705	EST	
38933	1	AA609606	Hs.112732	ESTs	
39894	1	H42037	Hs.144150	ESTs	
40244	1	H91660	Hs.30250	Homo sapiens short form transcription factor C-MAF (c-maf) mRNA complete cds	
40645	1	N47952	Hs.102624	EST	
40819	1	N63787	Hs.103304	ESTs	
41445	1	R45611	Hs.137696	ESTs Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	
41700	1	R85829	Hs.101883	EST	
41776	1	T03170	Hs.100165	EST	
13254	1	AA446587	Hs.6775	ESTs Highly similar to ALANINE AMINOTRANSFERASE [Homo sapiens]	
8171	1	AA362708	Hs.5009	ESTs Weakly similar to mTERF [H.sapiens]	
23030	1	T17291	Hs.6995	ESTs	
8406	1	AA427510	Hs.104287	ESTs	
16767	1	AA046650	Hs.40342	ESTs	
25010	1	AA005315	Hs.51262	ESTs	
14829	1	T35529	EST - T35529		
34584	1	AA280934	Hs.132872	ESTs Moderately similar to IIII ALU SUBFAMILY SC WARNING ENTRY IIII [H.sapiens]	
15909	1	Y07868	Hs.38842	H.sapiens mRNA for Pirm isolate 1	
9922	1	N44971	Hs.107164	Spectrin beta non-erythrocytic 1	
15381	1	W26496	Hs.107725	ESTs Weakly similar to LIS-1 protein [H.sapiens]	
22168	1	R53024	Hs.25985	ESTs	
11690	1	AA252762	Hs.31235	ESTs	
22989	1	T16510	Hs.6624	ESTs	
24490	1	Z38153	Hs.26921	ESTs	
19993	1	H91255	Hs.15227	ESTs	

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## FIGURE 7 (CONT.)

19889	1	H48825	Hs.36291	ESTs	
12450	1	AA401809	Hs.19865	ESTs	
24368	1	W87280	Hs.124800	ESTs	
22565	1	R77631	Hs.29126	ESTs	
18872	1	F10542	Hs.12292	ESTs	
15358	1	W26105	Hs.8961	ESTs	
24186	1	W61319	Hs.37482	ESTs Highly similar to COATOMER ZETA SUBUNIT [Bos taurus]	
23863	1	T93870	Hs.17265	ESTs	
23846	1	T93078	Hs.17117	EST	
15143	1	U79257	Hs.86921	Human clone 23932 mRNA sequence	
9711	1	L44334	Hs.10432	ESTs Weakly similar to BENOMYJ METHOTREXATE RESISTANCE PROTEIN [Candida albicans]	
22544	1	R74235	Hs.80844	Homo sapiens mRNA for KIAA0573 protein partial cds	
41506	1	R52088	EST - RC_R52088		
39345	1	C21105	Hs.7768	Homo sapiens FGF-1 intracellular binding protein (FIBP) mRNA complete cds	
22272	1	R58922	Hs.26590	ESTs	
16434	1	AA024494	Hs.61199	ESTs	
17255	1	AA084412	EST - RC_AA084412		
22692	1	R88711	Hs.34183	ESTs	
38830	1	AA609189	Hs.116415	ESTs	
9179	1	D50312	Hs.102308	Human mRNA for uKATP-1 complete cds	
42547	1	W73946	EST - RC_W73946		
36195	1	AA421144	EST - RC_AA421144		
29355	1	H70121	Hs.79592	ESTs	
34608	1	AA281765	Hs.104441	ESTs	
20779	1	N67553	Hs.16917	ESTs	
11081	1	AA149826	Hs.34274	ESTs	
12151	1	AA291269	Hs.24642	ESTs	
39935	1	H52379	EST - RC_H52379		
7157	1	AA037199	Hs.9899	ESTs	
17858	1	AA156596	Hs.72146	ESTs	
34885	1	AA302831	Hs.57732	Homo sapiens p38beta2 MAP kinase mRNA complete cds	
18445	1	AA232648	Hs.87068	ESTs	
22524	1	R72597	EST - RC_R72597		
19224	1	H12448	Hs.124570	ESTs Weakly similar to unknown protein [H.sapiens]	
18803	1	F09988	Hs.5244	ESTs	
13810	1	AA464689	Hs.23294	ESTs Weakly similar to weak similarity to HSP90 [C.elegans]	
18070	1	AA180352	Hs.72733	ESTs	
17937	1	AA164750	Hs.72499	ESTs	
39115	1	AA620736	Hs.112893	EST	
22517	1	R71892	Hs.25996	ESTs Highly similar to 40S RIBOSOMAL PROTEIN S27A [Homo sapiens Cavia porcellus]	

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## FIGURE 7 (CONT.)

16906	1	AA058555	Hs.63392	EST	
14251	1	AA497049	Hs.32501	ESTs	
23923	1	T96407	Hs.17812	ESTs	
21177	1	R06569	Hs.19721	ESTs	
25705	1	AA131921	Hs.71030	ESTs	
19805	1	H57725	Hs.124031	ESTs	
19668	1	H47656	Hs.33991	EST	
36993	1	AA432389	Hs.98702	ESTs	
14036	1	AA482107	Hs.5473	ESTs	
20859	1	N69825	Hs.16762	ESTs	
23849	1	T93113	EST - RC_T93113		
18265	1	AA207122	Hs.86316	ESTs	
35275	1	AA398530	Hs.97363	ESTs	
10262	1	R77869	Hs.110493	ESTs	
21757	1	R40789	Hs.21299	ESTs	
21541	1	R31607	Hs.24420	ESTs	
16873	1	AA056258	Hs.63264	EST	
19646	1	H46006	Hs.31677	ESTs	
23719	1	T89160	Hs.138506	ESTs	
19608	1	H41581	Hs.31582	ESTs	Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans]
17382	1	AA102731	Hs.109072	ESTs	
16864	1	AA055971	Hs.63238	ESTs	
10897	1	AA111801	Hs.9192	ESTs	
17028	1	AA070178	EST - RC_AA070178		
19220	1	H12318	Hs.24324	ESTs	
9726	1	L44574	Hs.125235	ESTs	
24570	0	Z38681	Hs.27150	ESTs	
22167	0	R53021	Hs.25873	ESTs	
42537	0	W73417	Hs.103183	EST	
18806	0	F10005	Hs.12599	ESTs	
16585	0	AA033948	Hs.4236	ESTs	
17309	0	AA086232	Hs.68717	EST	Moderately similar to mariner transposase [H.sapiens]
22813	0	R97419	Hs.35718	ESTs	
16429	0	AA022953	Hs.61172	EST	
22013	0	R46526	Hs.25377	EST	
8439	0	AA431277	Hs.32419	ESTs	
22934	0	T10042	Hs.4205	ESTs	
13063	0	AA432386	Hs.1191	Human mRNA for KIAA0073 gene partial cds	
10122	0	R31745	EST - R31745		
18195	0	AA195263	Hs.86001	EST	



## FIGURE 7 (CONT.)

33249	0	W7257	Hs.57836	ESTs
16966	0	AA063378	Hs.144270	ESTs
18363	0	AA223929	Hs.86902	EST
34154	0	AA219304	Hs.74561	ALPHA-2-MACROGLOBULIN PRECURSOR
16222	0	AA011210	Hs.95044	ESTs
17174	0	AA079306	EST - RC_AA079306	

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Primary Key	fold upregulated of tumor over normal	Accession	Unigene Descriptor	ORF structural info
16074	>10	AA001507	ESTs	other
25047	>10	AA011031	ESTs	other
25062	>10	AA017257	ESTs	other
16490	>10	AA026418	ESTs	other
25179	>10	AA031268	H.sapiens mRNA for kinasin-2	other
25215	>10	AA035540	APOLIPOPROTEIN AI REGULATORY PROTEIN-1	other
25282	>10	AA044825	ESTs	other
16810	>10	AA053636	ESTs	other
16835	>10	AA054438	ESTs	SS,
10747	>10	AA055841	ESTs	other
10748	>10	AA055892	ESTs	other
16993	>10	AA055300	Human mRNA for KIAA0035 gene partial cds	other
17051	>10	AA070801	ESTs	TM
10840	>10	AA084104	ESTs	other
7296	>10	AA085661	ESTs	other
7325	>10	AA090842	ESTs Weakly similar to HYPOTHETICAL 30.7 KD PROTEIN C2F7.02C IN CHROMOSOME 1 [Schizosaccharomyces pombe]	other
17419	>10	AA113349	EST	?
17541	>10	AA127459	ESTs	other
17559	>10	AA128407	ESTs	other
25669	>10	AA128978	ESTs	?
17600	>10	AA130596	ESTs	other
10992	>10	AA132523	Homo sapiens BAC clone RG119C02 from 7p15	other
17654	>10	AA133250	ESTs	TM
17734	>10	AA137246	ESTs	other
25801	>10	AA148530	EST - RC_AA148530	TM
25806	>10	AA149007	EST	?
11121	>10	AA156359	Human TAR DNA-binding protein-43 mRNA complete cds	?
11180	>10	AA164289	ESTs	other
25925	>10	AA164464	ESTs Weakly similar to CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 [H.sapiens]	other
25934	>10	AA165355	Human clone iota unknown protein mRNA complete cds	?
17987	>10	AA169379	ESTs	other
18008	>10	AA171895	Homo sapiens clone 24749 and 24750 mRNA sequences	TM
33953	>10	AA173290	Human HOXA1 mRNA long transcript and alternatively spliced forms complete cds	other
33980	>10	AA180223	CAMP-DEPENDENT PROTEIN KINASE TYPE II- ALPHA REGULATORY CHAIN	other
34013	>10	AA190888	EST - RC_AA190888	other
34014	>10	AA191348	ESTs	other
34015	>10	AA191353	ESTs	TM
34070	>10	AA196549	ESTs	other
18260	>10	AA205801	ESTs	?
34105	>10	AA207123	ESTs	SS,
34107	>10	AA209469	ESTs	other
18330	>10	AA216722	Human mRNA for apolipoprotein E receptor 2 complete cds	TM
18362	>10	AA223912	Ribonuclease L (2'-5'-oligoadenylate synthetase- dependent) inhibitor	other
18392	>10	AA227751	ESTs	SS,
34188	>10	AA228030	ESTs	TM
34197	>10	AA232315	Homo sapiens clone 23797 and 23817 mRNA partial cds	other
25948	>10	AA234365	Homo sapiens survival of motor neuron protein interacting protein 1 (SIP1) mRNA complete cds	?
25951	>10	AA234556	EST	?

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11581	>10	AA236533	Evi-1	other
26059	>10	AA236685	ESTs	other
26100	>10	AA242835	Human mRNA for KIAA0391 gene complete cds	other
11603	>10	AA243052	ESTs Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [Rattus norvegicus]	other
7785	>10	AA243375	EST - AA243375	other
34372	>10	AA251873	ESTs	?
26240	>10	AA252282	Human mRNA for KIAA0152 gene complete cds	TM
34382	>10	AA252512	ESTs	other
34391	>10	AA252703	EST - RC_AA252703	other
26274	>10	AA253011	ESTs	?
34400	>10	AA253400	ESTs	other
28291	>10	AA253422	ESTs	?
26355	>10	AA256379	ESTs	other
11813	>10	AA258158	ESTs	other
34518	>10	AA278721	ESTs	?
26545	>10	AA278979	ESTs	other
26574	>10	AA279504	ESTs	other
34554	>10	AA280016	DNA polymerase gamma	other
34561	>10	AA280298	ESTs	TM
26628	>10	AA280641	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L39 [Rattus norvegicus]	TM
11969	>10	AA280670	ESTs	SS
34575	>10	AA280738	ESTs	TM
26677	>10	AA281636	ESTs	?
26700	>10	AA282187	EST	?
34672	>10	AA284372	ESTs	other
34692	>10	AA285079	ESTs	other
12143	>10	AA290991	ESTs	other
8092	>10	AA316272	ESTs	TM
34904	>10	AA321746	EST	other
8111	>10	AA323787	ESTs	other
8125	>10	AA330771	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence	TM
26916	>10	AA331383	ESTs	other
26926	>10	AA342402	ESTs	other
26935	>10	AA347193	ESTs Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 [Caenorhabditis elegans]	TM
35038	>10	AA350541	ESTs Moderately similar to URACIL-DNA GLYCOSYLASE 1 PRECURSOR [H.sapiens]	TM
35049	>10	AA350657	ESTs	other
35106	>10	AA371561	EST Weakly similar to putative p150 [H.sapiens]	?
35197	>10	AA398120	ESTs	other
35277	>10	AA398536	ESTs	other
35309	>10	AA398660	EST	other
35322	>10	AA398710	H. sapiens RNA for CLCH3	TM
27037	>10	AA400198	ESTs	TM
35495	>10	AA400527	ESTs	?
27046	>10	AA400670	Homo sapiens mRNA for KIAA0582 protein partial cds	other
35500	>10	AA400715	ESTs	other
12480	>10	AA403116	Homo sapiens U-snRNP-associated cyclophilin (USA-CyP) mRNA complete cds	other
35693	>10	AA405485	ESTs Weakly similar to similar to 1 complex testis-specific protein [C. elegans]	other
35697	>10	AA405512	ESTs	other
35766	>10	AA406169	Homo sapiens KIAA0431 mRNA partial cds	other
35769	>10	AA406206	ESTs	other
35798	>10	AA410231	ESTs	other

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35801	>10	AA410291	ESTs	other
35803	>10	AA410295	ESTs	other
35822	>10	AA411144	ESTs	TM
35874	>10	AA412024	EST	?
35958	>10	AA412550	ESTs	other
36052	>10	AA417027	EST	TM
36258	>10	AA423962	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	other
36288	>10	AA424502	ESTs	other
36307	>10	AA424803	EST	?
36371	>10	AA426017	ESTs	TM
36395	>10	AA426353	ESTs	other
36405	>10	AA426406	Homo sapiens mRNA for KIAA0530 protein partial cds	other
36506	>10	AA429610	ESTs	other
36571	>10	AA430726	EST - RC_AA430726	SS.
36695	>10	AA433910	ESTs	other
36739	>10	AA435610	EST - RC_AA435610	?
36753	>10	AA435686	ESTs	other
36845	>10	AA436198	ESTs	?
13136	>10	AA436560	ESTs	SS, TM
13143	>10	AA436619	ESTs	SS.
36958	>10	AA442060	ESTs	other
36962	>10	AA442062	ESTs	?
36981	>10	AA442845	EST	?
13237	>10	AA443971	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	?
13242	>10	AA445994	ESTs	other
37057	>10	AA446131	ESTs	other
37068	>10	AA446312	ESTs Weakly similar to !!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]	other
37074	>10	AA446344	ESTs	SS.
37084	>10	AA446486	Homo sapiens Ran binding protein 2 (RanBP2alpha) mRNA partial cds	?
37135	>10	AA447540	EST	?
37159	>10	AA447714	EST - RC_AA447714	other
37168	>10	AA447772	ESTs	?
37246	>10	AA449311	Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds	other
37310	>10	AA451707	ESTs	other
37453	>10	AA454610	ESTs	?
37456	>10	AA454632	ESTs	TM
27787	>10	AA454660	ESTs	?
37492	>10	AA455248	EST - RC_AA455248	other
37546	>10	AA456641	ESTs	TM
37601	>10	AA458864	ESTs	other
37611	>10	AA458996	Human signaling lymphocyte activation molecule (SLAM) mRNA complete cds	SS, TM
37615	>10	AA459101	Human serine/threonine kinase mRNA partial cds	other
37653	>10	AA460017	ESTs	other
37677	>10	AA460530	Homo sapiens orphan G protein-coupled receptor HG38 mRNA complete cds	other
37777	>10	AA464860	Homo sapiens Jak2 kinase mRNA complete cds	other
8648	>10	AA465016	Homo sapiens serine protease-like protease (nest1) mRNA complete cds	?
37816	>10	AA469954	EST	?
37829	>10	AA470084	ESTs	other
28015	>10	AA477421	ESTs	other
37978	>10	AA479294	EST - RC_AA479294	other
37979	>10	AA479295	ESTs Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]	other

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37983	>10	AA478348	H sapiens mRNA for SYT	other
14054	>10	AA485223	ESTs	TM
38121	>10	AA485724	EST - RC_AA485724	other
28122	>10	AA485928	ESTs Weakly similar to LOK (M.musculus)	other
38167	>10	AA487207	EST - RC_AA487207	other
38172	>10	AA487424	EST - RC_AA487424	other
38179	>10	AA487492	Homo sapiens clone 23592 mRNA sequence	other
38182	>10	AA487501	ESTs	other
38184	>10	AA487969	ESTs	other
28141	>10	AA488432	ESTs	?
38211	>10	AA488687	ESTs	other
38235	>10	AA489030	ESTs	other
38280	>10	AA489791	EST - RC_AA489791	other
38316	>10	AA490500	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds	other
38330	>10	AA490882	ESTs	other
38456	>10	AA504343	ESTs	SS.
38460	>10	AA504462	ESTs	other
38553	>10	AA521471	ESTs	other
38580	>10	AA598545	ESTs	?
38590	>10	AA598648	Human mRNA for transcriptional activator hSNF2b complete cds	other
39601	>10	AA598738	ESTs	?
28323	>10	AA599639	ESTs	other
38828	>10	AA609177	ESTs	TM
38838	>10	AA609215	EST - RC_AA609215	?
38867	>10	AA609318	Human cbl-b mRNA complete cds	TM
38871	>10	AA609333	EST	?
38970	>10	AA609749	ESTs	other
38984	>10	AA609830	ESTs Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	?
39045	>10	AA610077	ESTs	other
39062	>10	AA620333	EST	?
39080	>10	AA620552	EST - RC_AA620552_f	?
39110	>10	AA620709	ESTs Weakly similar to HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II [C.elegans]	other
39178	>10	AA621091	ESTs	other
39218	>10	AA621330	ESTs	other
39221	>10	AA621346	Homo sapiens protein phosphatase with EF-hands-1 (PPEF-1) mRNA complete cds	other
39232	>10	AA621409	ESTs	other
21	>10	AB000905	H.sapiens histone H4 gene	?
8963	>10	AFFX-HUMTFRRM11507	AFFX-HUMTFRRM11507_M	?
33890	>10	AFFX-HUMTFRRM11507	AFFX-HUMTFRRM11507_5	?
39302	>10	C14944	ESTs	other
39329	>10	C20797	EST	?
28844	>10	D12163	ESTs	other
218	>10	D13540	PROTEIN-TYROSINE PHOSPHATASE 2C	other
236	>10	D13645	Human mRNA for KIAA0020 gene complete cds	other
9127	>10	D30037	PHOSPHATIDYLINOSITOL	other
459	>10	D38293	Human mRNA for clathrin-like protein complete cds	TM
39405	>10	D50975	ESTs	other
39433	>10	D52037	Human thymidine kinase 2 (TK2) mRNA complete cds	other
39436	>10	D52692	Human Ca2+-dependent activator protein for secretion mRNA complete cds	TM
14708	>10	D59388	EST	?

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39488	>10	D60631	ESTs	other
39504	>10	D80632	ESTs	other
765	>10	D86096	Prostaglandin E receptor 3 (subtype EP3) (alternative products)	?
787	>10	D86969	Human mRNA for KIAA0215 gene complete cds	other
789	>10	D86971	Human mRNA for KIAA0217 gene partial cds	other
39529	>10	F02202	ESTs	?
39535	>10	F02450	ESTs Moderately similar to unknown protein [H.sapiens]	TM
18678	>10	F04022	ESTs	other
18718	>10	F04915	ESTs	other
18762	>10	F09458	ESTs	other
18782	>10	F09739	ESTs	other
29080	>10	F13655	ESTs Moderately similar to [H] ALU SUBFAMILY SB1 WARNING ENTRY !!! [H.sapiens]	other
19001	>10	H02890	ESTs	other
19164	>10	H10395	EST	?
39725	>10	H11323	ESTs	other
19203	>10	H11593	ESTs	other
19328	>10	H17808	ESTs	other
19387	>10	H20128	ESTs	?
39787	>10	H20131	ESTs	SS,
19389	>10	H20185	EST	?
39832	>10	H26279	EST - RC_H26279	other
19591	>10	H40688	ESTs	other
29229	>10	H48459	Human mRNA for KIAA0186 gene complete cds	other
19727	>10	H52702	ESTs	?
19787	>10	H56679	ESTs	other
39895	>10	H62474	EST	SS, TM
29331	>10	H68116	ESTs	TM
29344	>10	H68839	EST	?
40064	>10	H72283	Human mRNA for KIAA0265 gene partial cds	other
40083	>10	H73466	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3	other
19949	>10	H78263	ESTs	TM
40204	>10	H88296	EST - RC_H88296	other
29523	>10	H88353	ESTs Weakly similar to bna-1 protein ORF2 [H.sapiens]	?
29551	>10	H90134	ESTs	?
29645	>10	H95840	ESTs	?
20057	>10	H98079	ESTs	other
976	>10	HG2036-HT2090	EST - HG2036-HT2090	?
1158	>10	HG3344-HT3521	EST - HG3344-HT3521	?
1210	>10	HG37-HT37	EST - HG37-HT37	?
1346	>10	HG4718-HT5158	EST - HG4718-HT5158	?
1349	>10	HG4747-HT5195	EST - HG4747-HT5195	?
1445	>10	J03027	MHC class I protein HLA-G	?
1570	>10	K01383	EST - K01383	?
1884	>10	L07541	Replication factor C (activator 1) 3 (38kD)	other
1852	>10	L17328	Human FEZ2 mRNA partial cds	TM
1856	>10	L18820	MELANOMA-ASSOCIATED ANTIGEN 2	?
1863	>10	L19161	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT	other
2070	>10	L37378	Homo sapiens guanylyl cyclase (RetGC-2) mRNA complete cds	SS, TM
2123	>10	L40395	Homo sapiens (clone #2271) mRNA fragment	other
2144	>10	L41349	Phospholipase C beta 4	SS,
9723	>10	L44542	ESTs	other
2188	>10	L47276	EST - L47276	other

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2343	>10	M15353	Eukaryotic translation initiation factor 4E	other
2627	>10	M29610	Glycophorin E	TM
2657	>10	M58597	Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific)	TM
3021	>10	M58941	Protein tyrosine phosphatase non-receptor type 4	other
3163	>10	M84424	Cathepsin E	?
3196	>10	M85917	Oryzasterol binding protein	other
20088	>10	N20054	ESTs Weakly similar to putative p150 [H.sapiens]	?
29785	>10	N20641	ESTs Highly similar to HYPOTHETICAL MYELOID CELL LINE PROTEIN 3 [Homo sapiens]	other
40427	>10	N21147	ESTs	other
40444	>10	N22140	ESTs Highly similar to TUBULIN GAMMA CHAIN [Euplexia octocarinatus]	other
29893	>10	N23003	ESTs	TM
40458	>10	N26086	Homo sapiens citrate synthase mRNA complete cds	SS
40559	>10	N33024	ESTs	SS
30190	>10	N33264	EST	?
30207	>10	N33920	H.sapiens mRNA for ubiquitin	other
20304	>10	N34688	Homo sapiens clone 23915 mRNA sequence	?
20307	>10	N34830	ESTs	other
30285	>10	N35115	ESTs	other
40594	>10	N35388	ESTs	other
40604	>10	N36893	Homo sapiens KIAA0428 mRNA complete cds	other
40631	>10	N45124	ESTs	other
40660	>10	N49104	NUCLEAR FACTOR RIP140	other
30610	>10	N50138	EST	?
30617	>10	N50646	ESTs	other
30631	>10	N50807	EST	?
30780	>10	N52935	EST	?
20564	>10	N55443	ESTs	TM
40760	>10	N57927	ESTs Weakly similar to ELL [M.musculus]	other
30938	>10	N58561	Cathepsin B	other
20614	>10	N58230	ESTs	SS
20657	>10	N62889	ESTs	other
31136	>10	N63512	ESTs Weakly similar to MD1F1.4 [C.elegans]	TM
40827	>10	N54051	Homo sapiens Werner syndrome gene complete cds	other
31310	>10	N66831	EST	?
40876	>10	N67607	Human Rho-associated coiled-coil containing protein kinase p16OROCK mRNA complete cds	other
20791	>10	N68057	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds	?
40905	>10	N68738	ESTs	other
40911	>10	N69114	H.sapiens mRNA for orphan nuclear hormone receptor	other
40913	>10	N69218	ESTs	other
31484	>10	N69466	ESTs	other
31618	>10	N73449	ESTs	other
41005	>10	N79516	ESTs	TM
31818	>10	N89774	Homo sapiens mRNA for KIAA0292 gene partial cds	other
31872	>10	N91109	EST	other
41040	>10	N91948	ESTs	other
31944	>10	N93193	ESTs	other
41065	>10	N93618	ESTs	other
32034	>10	N98926	ESTs Moderately similar to DMR-N9 PROTEIN [H.sapiens]	other
41107	>10	R01634	ESTs	other
41163	>10	R08176	ESTs	other
21238	>10	R08564	Plasminogen-like protein	other

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21240	>10	R08613	ESTs	other
21412	>10	R20670	ESTs	other
21519	>10	R27975	EST - RC_R27975	other
41381	>10	R42278	H sapiens mRNA for TRE5	?
32189	>10	R43183	ESTs	TM
32195	>10	R43471	ESTs Weakly similar to ORF YOR258w [S.cerevisiae]	other
21902	>10	R43822	EST	?
21946	>10	R44707	ESTs	TM
22072	>10	R49405	ESTs	?
32240	>10	R50976	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor	other
32258	>10	R55823	ESTs	other
22258	>10	R56432	ESTs	other
22282	>10	R58197	ESTs	other
32277	>10	R61493	Human mRNA for rod photoreceptor protein complete cds	other
22372	>10	R62831	EST	?
22400	>10	R64109	ESTs	other
41593	>10	R64129	ESTs	other
10233	>10	R71427	ESTs Highly similar to PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN CYTOPLASMIC [Saccharomyces cerevisiae]	other
41654	>10	R76437	THROMBOXANE-A SYNTHASE	TM
22557	>10	R76722	ESTs	other
22576	>10	R79111	ESTs	other
22593	>10	R79777	EST	?
41678	>10	R80675	EST	?
41719	>10	R89260	EST - RC_R89260	other
22793	>10	R96208	ESTs	other
41752	>10	R97063	ESTs	other
3375	>10	S50223	HKR-T1	other
3406	>10	S66896	SQUAMOUS CELL CARCINOMA ANTIGEN 1	other
3522	>10	S80267	Spleen tyrosine kinase	other
41793	>10	T03887	ESTs	?
23198	>10	T40530	ESTs Weakly similar to B0035.14 [C.elegans]	other
23360	>10	T58531	ESTs	other
32635	>10	T61116	ESTs	other
42177	>10	T79786	ESTs	?
23623	>10	T84047	ESTs	?
23662	>10	T86674	ESTs	other
42242	>10	T89579	Human spleen E2F-related transcription factor (DP-1) mRNA complete cds	other
23759	>10	T90313	ESTs	other
23832	>10	T92018	ESTs	other
32740	>10	T92950	ESTs	other
42290	>10	T95105	ESTs	?
3598	>10	U01157	Glucagon-like peptide-1 receptor	SS, TM
3659	>10	U04313	Protease inhibitor 5 (maspin)	other
3799	>10	U10690	Human MAGE-5a antigen (MAGE5a) gene complete cds	?
3870	>10	U14518	Centromere protein A (17kD)	other
3913	>10	U16261	Human MDA-7 (mda-7) mRNA complete cds	SS,
4029	>10	U21090	Human DNA polymerase delta small subunit mRNA complete cds	other
4157	>10	U28811	Human cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA complete cds	other
4178	>10	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	TM
15006	>10	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	TM

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4193	>10	U31116	Human beta-as/coglycan A3b mRNA complete cds	TM
4306	>10	U36798	Homo sapiens platelet cG1-PDE mRNA complete cds	TM
4382	>10	U39817	Bloom syndrome	other
4386	>10	U40822	DNA repair protein XRCC4	other
4388	>10	U40714	Human tyrosyl-tRNA synthetase mRNA complete cds	other
4455	>10	U43944	MALATE OXIDOREDUCTASE	other
4477	>10	U45880	Human IAP-like protein ILP mRNA complete cds	other
4680	>10	U55766	Human Rev interacting protein Rip-1 mRNA complete cds	TM
4702	>10	U57341	EST - U57341	other
4713	>10	U57721	Human L-tyrosine hydrolase mRNA complete cds	other
4787	>10	U61145	Human enhancer of zeste homolog 2 (EZH2) mRNA complete cds	other
4862	>10	U65437	Human homeodomain-containing protein (HANF) mRNA complete cds	?
4945	>10	U69108	Homo sapiens mRNA for TRAF5 complete cds	other
4975	>10	U71088	Human MEK5 mRNA complete cds	other
4994	>10	U72514	Human C2f mRNA complete cds	other
5002	>10	U72761	Human karyopherin beta 3 mRNA complete cds	other
5021	>10	U73524	Human putative ATP/GTP-binding protein (HEAB) mRNA complete cds	TM
5149	>10	U79716	Human reelin (RELN) mRNA complete cds	SS,
5214	>10	U83303	H.sapiens mRNA for granulocyte chemotactic protein	?
5243	>10	U85946	Human brain secretory protein hSec10p (HSEC10) mRNA complete cds	other
32789	>10	V02779	ESTs Moderately similar to kinesin-73 (D.melanogaster)	other
42354	>10	VH9346	ESTs	other
42390	>10	W40150	Homo sapiens chromosome-associated polypeptide (HCAP) mRNA complete cds	other
33006	>10	W46286	ESTs Weakly similar to ZK1058.5 [C.elegans]	TM
33020	>10	W46891	ESTs Weakly similar to polypeptide N-acetylglucosaminyltransferase [H.sapiens]	other
33109	>10	W59961	Human mRNA for KIAA0389 gene complete cds	other
24197	>10	W67277	ESTs	other
24215	>10	W69425	ESTs	other
33301	>10	W73683	ESTs	other
33343	>10	W79834	ESTs Weakly similar to rhotekin [M.musculus]	other
33377	>10	W81219	ESTs Weakly similar to F45B6.7 [C.elegans]	other
42602	>10	W86423	ESTs	TM
33556	>10	W90705	Murine leukemia viral (bmi-1) oncogene homolog	other
33616	>10	W93726	Protease inhibitor 5 (maspin)	other
33666	>10	W95876	ESTs	TM
5510	>10	X05360	Cell division cycle 2 G1 to S and G2 to M	?
5558	>10	X07876	Wingless-type MMTV integration site 2 human homolog	SS,
5603	>10	X14253	Taralocarcinoma-derived growth factor 1	TM
5619	>10	X14850	HISTONE H2A X	SS,
5623	>10	X14975	T-CELL SURFACE GLYCOPROTEIN CD1E PRECURSOR	?
5692	>10	X17644	G1 to S phase transition 1	other
5789	>10	X54925	Matrix metalloproteinase 1 (interstitial collagenase)	other
5799	>10	X55330	Aspartylglucosaminidase	SS,
5802	>10	X55544	CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-1	?
5857	>10	X58377	Human mRNA for adipo genesis inhibitory factor	other
5960	>10	X63575	ATPase Ca++ transporting plasma membrane 2 (NOTE: redefinition of symbol)	TM
5963	>10	X63629	Cadherin 3 (P-cadherin)	SS, TM
5986	>10	X64810	Protein convertase subtilisin/kexin type 1	?
6041	>10	X67155	MITOTIC KINESIN-LIKE PROTEIN-1	other
6095	>10	X69962	Fragile X mental retardation 1	other

FIGURE 8 (cont.)

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6106	>10	X70683	SRY (sex determining region Y)-box 4	TM
6155	>10	X74331	DNA primase polypeptide 2A (58kD)	other
6167	>10	X74987	Robonuclease L (2'S'-oligoisoadenylate synthetase-dependent) inhibitor	other
6188	>10	X76029	NEUROMEDIN U-25 PRECURSOR	TM
6315	>10	X81889	H.sapiens mRNA for p0071 protein	other
6382	>10	X85133	H.sapiens RBO-1 mRNA	other
6384	>10	X85137	Human kinesin-like spindle protein HKSP (HKSP)	other
6438	>10	X89398	mRNA complete cds URACIL-DNA GLYCOSYLASE 1 PRECURSOR	?
6440	>10	X89986	H.sapiens mRNA for NBK apoptotic inducer protein	TM
6478	>10	X91648	H.sapiens mRNA for pur alpha extended 3' untranslated region	SS, TM
6479	>10	X91653	EST - X91653	?
6494	>10	X92689	H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylglucosaminyl transferase	TM
6713	>10	Y08564	EST - Y08564	?
6790	>10	Y12394	Homo sapiens importin-alpha homolog (SRP1 gamma)	other
24915	>10	YE003w	mRNA complete cds EST - YE003w	?
42773	>10	YE019c/MMS21	EST - YE019c/MMS21	?
24545	>10	Z38462	ESTs	other
33713	>10	Z39427	ESTs	other
33791	>10	Z40883	ESTs	other
42766	>10	Z99394	ESTs Moderately similar to !!! ALU SUBFAMILY SP WARNING ENTRY !!! [H.sapiens]	other
21558	>10	R33112	Human AF-6 mRNA complete cds	other
26718	>10	AA282576	ESTs	?
40113	9 9855090946	H78003	ESTs	?
10801	9 8979448276	AA069285	ESTs Weakly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 [C.elegans]	other
37491	9 9513600842	AA455239	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 [Caenorhabditis elegans]	other
23900	9 9272347693	T95789	ESTs	other
254	9 9198395324	D14657	Human mRNA for KIAA0101 gene complete cds	other
6885	9 8970927814	Z29331	Ubiquitin-conjugating enzyme E2H (homologous to yeast UBC8)	other
29693	9 8850766398	H97819	ESTs	SS,
26482	9 8765189024	AA262491	ESTs	other
23123	9 8699502035	T25306	EST	?
26525	9 8160399123	AA278392	ESTs	other
13110	9 7643356605	AA435840	Homo sapiens mRNA for high mobility group protein HMGB2a	other
34063	9 7087597628	AA299784	EST	other
39432	9 7034550063	D51691	Phosphoribosylglycinamide formyltransferase phosphoribosylglycinamide synthetase phosphoribosylformimidazole synthetase	?
31312	9 6513325388	N66845	ESTs Weakly similar to !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]	?
21112	9 6358446349	R01179	ESTs	?
31572	9 6254820695	N71294	ESTs	other
17903	9 6221229759	AA160259	EST	?
20747	9 6094813734	N66842	ESTs	other
4676	9 589223908	U55206	Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA complete cds	TM
34363	9 5627081023	AA251587	Homo sapiens mRNA for KIAA0530 protein partial cds	other
39094	9 540768988	AA620936	ESTs	other
3888	9 5372000133	U15128	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds	?
39386	9 506250529	D12184	ESTs	TM
7674	9 4458059039	AA203742	ESTs	other
4192	9 4329744134	U31099	Human DP prostanoid receptor (PTGDR) mRNA partial cds	TM
4507	9 422674945	U47050	Human putative calcium influx channel (htrp3) mRNA complete cds	TM

FIGURE 8 (cont.)

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35606	9.412026255	AA402227	ESTs Moderately similar to N-tropomodulin [R.norvegicus]	other
4970	9.3649551013	U70862	Human nuclear factor kappa B2 (NFkB2) mRNA complete cds	?
19829	9.3432151573	H58813	EST	?
14837	9.2878584141	T40145	ESTs	TM
17336	9.2822148675	AA099585	ESTs	other
40541	9.2532836505	N30160	ESTs	other
29498	9.2487843833	H85434	EST	?
29943	9.1797074262	N24766	ESTs Moderately similar to IIIA ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	TM
17897	9.1628681314	AA169633	EST	other
21320	9.1243463318	R11873	ESTs	other
13883	9.1178796537	AA476917	ESTs Weakly similar to No definition line found [C.elegans]	other
30539	9.0888887776	H49072	ESTs	other
32778	9.0877919549	W02063	EST	?
26380	9.0809559378	AA257012	EST	?
15888	9.0559893607	X95632	Human Abi interactor 2 (Abi-2) mRNA complete cds	other
40812	9.0012874244	N63419	ESTs	other
903	8.9640387908	D90070	ATL-derived PMA-responsive (APR) peptide	other
22874	8.9515777733	R87160	ESTs	TM
40807	8.9510132281	N62995	TRANSCRIPTION INITIATION FACTOR IIF BETA SUBUNIT	other
15244	8.9195644974	W00904	ESTs	TM
32786	8.8658776567	R87075	Zinc finger protein X-linked	other
18269	8.8575656769	AA209467	ESTs	other
19682	8.8507628284	H47391	ESTs	other
41607	8.83325517	R67868	CLEAVAGE SIGNAL-1 PROTEIN	other
2548	8.8299864699	M25897	Platelet factor 4	TM
7736	8.8279341243	AA232121	Human tyrosyl-tRNA synthetase mRNA complete cds	other
34490	8.7844537272	AA262354	ESTs	other
38658	8.7669313482	AA599477	ESTs	other
7528	8.765157554	AA149543	ESTs	other
39939	8.7555031142	H53454	EST - RC_H53454	other
25111	8.7232692309	AA020787	ESTs	other
21655	8.716167279	R38239	EST	?
39663	8.665982852	H04756	ESTs Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT [Bos taurus]	other
1042	8.652112324	HG2510-HT2806	EST - HG2510-HT2806	?
32330	8.6361115426	R77776	ESTs	other
25382	8.6239458487	AA059007	ESTs	other
27074	8.5900813078	AA401475	ESTs Weakly similar to C3681.3 [C.elegans]	SS,
3955	8.5298909183	U18259	MHC class II transactivator	other
4959	8.52646827	U70322	Human transporin (TRN) mRNA complete cds	other
2315	8.5259185808	M14123	EST - M14123_xp1	?
37253	8.4896914632	AA449357	ESTs	other
39624	8.471316977	F10836	ESTs	?
23213	8.4569920887	T40691	ESTs	?
2788	8.455509435	M54995	Connective tissue activation peptide III	TM
41154	8.4413390141	R07499	ESTs	?
32478	8.4093689549	T16282	WEE1-LIKE PROTEIN KINASE	other
41251	8.3587565415	R28279	Human clone 23548 mRNA sequence	other
19081	8.3583603183	H06701	ESTs Weakly similar to RHOMBOTIN-1 [H.sapiens]	other
21098	8.3105927559	R00545	ESTs	other
14723	8.3061679053	D59894	ESTs	other
37154	8.2994822341	AA447666	Human CENP-F kinetochore protein mRNA complete cds	other

FIGURE 8 (cont.)

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8068	8.2835506361	AA313387	ESTs Highly similar to HYPOTHETICAL 84.7 KD PROTEIN ZK1028.1 IN CHROMOSOME III (Caenorhabditis elegans)	other
7485	8.281679348	AA129547	ESTs	other
16501	8.2517969834	AA026869	ESTs	other
34527	8.2419163754	AA279091	ESTs	other
6700	8.1948675662	Y07867	H. sapiens mRNA for Pivn isolate 1	other
2852	8.1928816537	M58460	Human 754-D autoantigen (PM-Sc1) mRNA complete cds	other
11188	8.1862492468	AA172372	ESTs	TM
42293	8.183311064	T95333	ESTs Weakly similar to coded for by C. elegans cDNA yk110g8.3 (C. elegans)	TM
5443	8.1763317544	X02530	Interferon (gamma)-induced cell line protein 10 from	SS
40637	8.1534810594	N70607	ESTs	TM
23371	8.1499496068	T59505	EST - RC_T59505	?
26272	8.1339974519	AA252981	ESTs Weakly similar to K07C11.10 gene product (C. elegans)	other
17306	8.1332403762	AA086201	ESTs	other
18497	8.1192326373	AA233785	ESTs	other
235	8.0944363901	D13644	Human mRNA for KIAA0019 gene complete cds	other
24525	8.0860167097	Z38347	ESTs	TM
7826	8.0750029554	AA248884	EST - AA248884	TM
32142	8.0739258775	R38715	Homo sapiens clone 24540 mRNA sequence	other
39067	8.0557768803	AA620405	ESTs	other
6235	8.0448957236	X78416	Casein alpha S1	TM
29517	8.0017588725	H88261	ESTs	other
28570	7.9852455973	C21104	Homo sapiens STAT-induced STAT inhibitor-2 mRNA complete cds	other
30344	7.9162087762	C21034	ESTs Moderately similar to initiation factor eIF-2B gamma subunit (R.norvegicus)	other
18951	7.9002189759	H00580	ESTs	other
18953	7.8709160227	H00615	ESTs	other
18376	7.8564096918	AA226925	ESTs	other
19830	7.847878447	H58911	ESTs	other
36023	7.840835828	AA416881	ESTs	other
13347	7.8344414518	AA449238	ESTs	other
36614	7.8284591351	AA431466	ESTs	other
2192	7.8254072032	L48211	Homo Sapiens angiotensin II receptor gene complete cds	?
33016	7.8006574068	VV46577	H. sapiens mRNA for ESM-1 protein	other
17215	7.7941954038	AA083044	ESTs	other
34894	7.7659738105	AA311881	EST	?
40814	7.695001222	N39257	ESTs	other
38295	7.6834749699	AA424534	ESTs	other
19564	7.6744302788	H38833	ESTs	TM
18914	7.6686405336	AA058665	ESTs	SS
35967	7.6378079107	AA412694	Human splicing factor SRp55-2 (SRp55) mRNA complete cds	other
21672	7.6364823402	R38635	ESTs	other
19918	7.6303275831	H69787	ESTs	?
10511	7.6297744482	AA024482	ESTs Highly similar to KERATIN TYPE I CYTOSKELETAL 14 (Homo sapiens)	other
17721	7.6057911016	AA136590	ESTs	?
42302	7.6031859697	T96130	EST	SS
26134	7.6000619363	AA243763	ESTs	other
18766	7.5621799008	F09497	ESTs	other
34492	7.501590494	AA262439	ATL-derived PMA-responsive (APR) peptide	other
270	7.4512152125	D14822	EST - D14822	other
35975	7.4177746986	AA412738	ESTs	other
29842	7.4085808671	N21688	ESTs	?

FIGURE 8 (cont.)

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35389	7.3913043319	AA399555	ESTs	other
19979	7.3868157166	H88477	ESTs	other
5793	7.3655664025	X54942	CDC28 protein kinase 2	other
18978	7.380969715	H87770	EST - RC_H87770	other
1280	7.3691089318	HG4126-HT4396	EST - HG4126-HT4396	?
31571	7.3676263454	H71250	ESTs	other
23765	7.3541191734	T90443	ESTs Weakly similar to KIAA0376 [H.sapiens]	?
35123	7.3397933455	AA380927	EST	?
38252	7.3341119467	AA489247	ESTs	other
38218	7.3282021037	AA488861	ESTs	other
29418	7.2489407005	H77915	EST - RC_H77915	?
4834	7.1980951054	U63541	Human mRNA expressed in HCC/HCC livers and MolT-4 proliferating cells partial sequence	other
42504	7.1913036522	W69803	ESTs	other
6111	7.158000198	X71125	H. sapiens mRNA for glutamine cyclotransferase	TM
41773	7.154478618	T03024	ESTs Weakly similar to ribosomal protein L7 [H.sapiens]	other
9951	7.1363626365	N71513	ESTs	other
28109	7.0941968224	AA485212	ESTs	other
988	7.0783044659	HG2150-HT2230	EST - HG2150-HT2230	?
29848	7.0610668511	N22107	ESTs	other
30528	7.0607950168	N50744	ESTs	other
22587	7.0225726353	R77771	ESTs	TM
9347	7.006323071	H03686	ESTs	TM
11696	7.0026773299	AA252894	ESTs	other
40584	7.0010096333	N34870	EST	?
193	6.9767029188	D10923	PROBABLE G PROTEIN-COUPLED RECEPTOR HM74	TM
18305	6.9740536051	AA214048	Collagen type IV alpha 4	other
6078	6.9699682397	X69141	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE	other
26741	6.902658703	AA283198	ESTs	other
35069	6.8997885685	AA358397	EST	?
23504	6.8977135983	T71042	ESTs	other
299	6.8824513029	D16815	Human sapiens orphan nuclear hormone receptor BD73 mRNA 3' end	other
40583	6.8689903023	N34855	ESTs	other
31428	6.8623762224	N68594	ESTs	other
6169	6.8606959727	X75091	SET PROTEIN	other
39524	6.8567356171	F01905	MALATE OXIDOREDUCTASE	other
34578	6.8430889439	AA280837	ESTs	other
38678	6.837527995	AA599920	Small inducible cytokine A5 (RANTES)	other
23936	6.8251471804	T96930	ESTs	other
9326	6.8181321394	D89377	Msh (Drosophila) homeo box homolog 2	other
19188	6.8067351958	H11255	ESTs Highly similar to ACTIN-LIKE PROTEIN [Bos taurus]	TM
18185	6.7882148811	AA194983	Human sapiens mRNA for osteoclastogenesis inhibitory factor (OCIF) complex cds	other
27028	6.757529124	AA399630	ESTs Weakly similar to KIAA0371 [H.sapiens]	other
41289	6.7519531681	R37265	EST	other
34511	6.7364448798	AA278298	EST - RC_AA278298	other
1566	6.7056207716	J05614	EST - J05614	?
25675	6.6692299748	AA129757	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]	other
5814	6.6584342828	X56088	CYTOCHROME P450 VII	SS
13861	6.6238291607	AA470145	ESTs	other
29794	6.6026313352	N20568	ESTs	other
39333	6.5902382643	C20810	Cyclin B1	other
3770	6.5835303599	U09609	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p48/p100)	other

FIGURE 8 (cont.)

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31831	6.5829933764	N89894	ESTs	?
33063	6.5808125026	V63000	Homo sapiens clone 24431 mRNA sequence	other
20326	6.5640084836	N35583	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 56]	?
34384	6.5535703492	AA252537	ESTs	other
25599	6.5490481991	AA114091	Human (clone 881) Br-cadherin mRNA complete cds	other
39749	6.5369363254	H14988	ESTs	other
42596	6.5200567072	V85900	ESTs	?
39606	6.5119482185	F10243	ESTs Weakly similar to H1 ALU CLASS 8 WARNING ENTRY III [H.sapiens]	?
14617	6.5103504748	C14983	ESTs	other
27831	6.45670814	AA456044	ESTs	?
34896	6.4496517783	AA312551	EST	?
27360	6.4434305006	AA425356	ESTs	other
20126	6.4326610424	N22015	ESTs	TM
6663	6.4324809977	Y00291	RETINOIC ACID RECEPTOR BETA-2	TM
30692	6.4196636207	N51583	ESTs	other
36472	6.4189542265	AA428633	EST	?
9578	6.3961788753	H87652	Homo sapiens bicucullin (BICD) mRNA complete cds	other
39670	6.3818496159	H05626	ESTs	other
22897	6.3652792447	R89218	ESTs	other
37308	6.3647804993	AA451694	EST	TM
16101	6.3517262802	AA002147	EST	?
20629	6.3486854401	N59798	ESTs	other
36100	6.3364146287	AA417740	ESTs	?
15488	6.3252580241	V028097	Homo sapiens clone 23711 unknown mRNA partial cds	other
36667	6.3131273544	AA432136	ESTs	other
30766	6.3115037824	N52627	EST - RC_N52627	?
32882	6.2745311453	V037683	ESTs	TM
18072	6.2675787205	AA180448	EST	?
18231	6.2652604863	AA199747	Human mRNA for KIAA0096 gene partial cds	other
38282	6.2514165678	AA489814	EST	?
28125	6.250317021	AA486073	ESTs	other
37464	6.2484456382	AA454747	ESTs	?
36618	6.1846328223	AA431478	ESTs	other
5082	6.1831116815	U78524	Human Gu binding protein mRNA partial cds	other
1441	6.1777287039	J02963	Integrin alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex antigen CD41B)	other
42105	6.14875944	T87710	ESTs	?
6061	6.1394863141	X68314	Glutathione peroxidase 2 gastrointestinal	SS
32570	6.1156028796	T30222	ESTs Weakly similar to tetracycline transporter-like protein [M.musculus]	TM
32504	6.1019612076	T17063	EST	?
23335	6.0977927504	T56804	EST	?
10667	6.0970991075	AA088458	ESTs Weakly similar to H1 ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	other
30863	6.0911993489	N56923	EST	?
14528	6.0859008453	AA620295	ESTs	TM
20454	6.0685955038	H81308	EST	?
6798	6.0539173278	Y13153	Homo sapiens mRNA for kynurenine 3-monooxygenase	TM
21248	6.0525426545	R08071	ESTs	?
21840	6.0499964138	R44538	ESTs	?
29096	6.0455247653	F10927	Homo sapiens clone 23636 mRNA sequence	other
18774	6.0446826953	F09609	ESTs	?
36722	6.0172343991	AA435512	ESTs	SS
18062	6.0034342969	AA179845	ESTs Moderately similar to rabiesin-6 [M.musculus]	other

FIGURE 8 (cont.)

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22989	5.9992817406	T16305	ESTs	other
41745	5.9905623398	R85895	ESTs	?
8787	5.9894877858	AA504307	X-LINKED HELICASE II	other
20550	5.984861795	N55013	ESTs	other
26470	5.9417764101	AA262179	ESTs	other
16574	5.9356497569	AA031926	EST	other
693	5.9169537385	D80007	Human mRNA for KIAA0185 gene partial cds	other
4093	5.914830973	U25182	Human antioxidant enzyme AOE37-2 mRNA complete cds	TM
1182	5.9086264407	HQ3546-HT3744	EST - HQ3546-HT3744	?
22856	5.8954735623	T10248	ESTs	other
36723	5.891608409	AA435524	EST	?
2114	5.8844986595	L40384	EST - L40384	other
26872	5.868238789	AA281137	ESTs	other
6602	5.8663883018	X98266	EST - X98266_cds2	other
42701	5.8594483433	Z38612	ESTs	other
28573	5.84591118	C21118	ESTs	other
18290	5.8189427595	AA211901	ESTs	other
732	5.8043917941	D83781	Human mRNA for KIAA0197 gene partial cds	other
5330	5.8014145811	U91327	EST - U91327	?
33503	5.7990715189	W68720	EST	?
2553	5.7787505864	M28167	Human platelet factor 4 variation 1 (PF4var1) gene complete cds	?
34705	5.7658806254	AA286907	ESTs Weakly similar to putative p150 [H.sapiens]	other
42865	5.76404091043	W93659	ESTs	other
38180	5.7539310793	AA487495	EST - RC_AA487495	other
4244	5.7476738809	U33286	Human chromosome segregation gene homolog CAS mRNA complete cds	other
32822	5.7418957453	W16834	ESTs	TM
3977	5.7245885557	U18991	Retinal pigment epithelium-specific protein (65kD)	?
24573	5.7202366155	Z39301	ESTs	TM
6928	5.7120261128	Z46629	SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversal)	other
38726	5.7030798258	AA608733	ESTs	?
39290	5.6892372058	C14573	Human mRNA for KIAA0029 gene partial cds	other
11405	5.6818873796	AA232231	ESTs	other
22538	5.6792008591	R73587	Homo sapiens meltrin-L precursor (ADAM12) mRNA complete cds	TM
40747	5.6605393208	N56872	Homo sapiens clone 22 mRNA alternative splice variant alpha-1 complete cds	TM
31586	5.6554024604	N72094	ESTs	other
6329	5.6415662518	X82279	EST - X82279	?
31578	5.6273323661	N71361	ESTs	other
33207	5.6271818482	W70051	H.sapiens mRNA for M-phase phosphoprotein mpp9	other
2545	5.6105860146	M25753	Cyclin B1	other
22580	5.5988402647	R79156	ESTs	other
33592	5.5935314518	W93127	ESTs	other
28643	5.5734698755	D60252	ESTs	other
6160	5.5689050619	X74794	CDC21 HOMOLOG	other
37987	5.561345667	AA479606	ESTs	other
42515	5.5217868811	W72116	Homo sapiens clone 23622 mRNA sequence	other
4732	5.5130668527	U58522	Human huntingtin interacting protein (HIP2) mRNA complete cds	other
3299	5.5099850678	M95623	Hydroxymethylglutathione synthase	?
28320	5.473405981	AA599574	ESTs	?
746	5.471260899	D84454	Human mRNA for UDP-galactose translocator complete cds	TM
39373	5.4635804954	C21517	ESTs	other
3117	5.4398413537	M81182	Peroxisomal membrane protein 1 (70kD Zellweger syndrome)	other

FIGURE 8 (cont.)

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21257	5.4343612441	R09190	ESTs Moderately similar to M-phase phosphoprotein 11 [H.sapiens]	other
31487	5.4318648859	N69507	ESTs	other
28954	5.4137130511	F03153	ESTs	other
38928	5.389782721	AA809595	ESTs	other
29903	5.372320622	N23366	EST	?
30925	5.3437432315	N58295	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]	?
19091	5.3344615869	H07864	ESTs	TM
28209	5.3138951918	AA491250	ESTs	other
9470	5.3118897984	H46617	EST - H46617	other
9435	5.3070056656	H30201	EST - H30201	?
28552	5.2954432572	C20914	ESTs	other
27411	5.2940164267	AA428137	ESTs	other
30615	5.2924125264	N50556	ESTs	other
28313	5.2857977187	AA599309	ESTs	TM
39321	5.2649035384	C20632	ESTs	?
29934	5.2531047395	N24194	ESTs	other
1094	5.2496703122	HG2846-HT2983	EST - HG2846-HT2983	?
39578	5.2481126384	F08925	ESTs	TM
11232	5.2468798424	AA186804	ESTs Weakly similar to unknown [S.cerevisiae]	other
2468	5.2426349328	M21539	Human small proline rich protein (spr1) mRNA clone 1292	other
26843	5.2387758661	AA287450	ESTs	?
40331	5.2353385567	H97562	ESTs Weakly similar to SPERMATID-SPECIFIC PROTEIN T2 [Sapiens officinalis]	other
8035	5.205798365	AA305116	EST - AA305116	other
29783	5.1955425722	N20593	ESTs Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]	other
34109	5.1481590107	AA210722	EST	?
26408	5.1432577257	AA258177	ESTs Weakly similar to ROSA26AS [M.musculus]	other
19263	5.1427029807	H15054	ESTs	TM
24596	5.1416089352	Z38810	ESTs	other
28589	5.1385059753	C21245	H.sapiens mRNA for apoptosis specific protein	other
5684	5.1121931412	X17098	Pregnancy-specific beta-1 glycoprotein 6	other
30710	5.1079347344	N51761	EST	?
35765	5.0973514948	AA406167	EST	?
26360	5.0863127861	AA256460	ESTs	?
2351	5.0849612092	M15796	Proliferating cell nuclear antigen	?
30262	5.0836877534	N35065	Homo sapiens clone 24739 mRNA sequence	other
41782	5.0737512465	T03886	ESTs	?
36710	5.0703839864	AA434411	ESTs	other
39090	5.0546885407	AA820828	ESTs	TM
42185	5.0539926381	T79951	ESTs	?
18745	5.0460321557	F09134	ESTs	other
35746	5.0396841996	AA406063	ESTs	other
35356	5.0354809581	AA399053	EST	?
36769	5.0312706878	AA435750	EST	?
36900	5.0279911540	AA436866	H.sapiens mRNA for M-phase phosphoprotein mpp9	other
27595	5.0244757301	AA443328	ESTs	TM
16290	5.0056611904	AA016145	ESTs	?
27117	5.0018146599	AA405098	ESTs Weakly similar to MOESIN/VEZRN/RADIXIN HOMOLOG [D.melanogaster]	other
4304	4.9951954397	U36764	Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit	other
33458	4.9907402071	V85835	Homo sapiens mRNA for KIAA0636 protein complete cds	other
26680	4.9800090679	AA282120	EST	?
12669	4.9758138651	AA417030	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds	other

FIGURE 8 (cont.)

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29701	4 9708526387	H97970	EST	?
20480	4.8557253636	N52168	ESTs	TM
8720	4 9439110602	AA481218	EST - AA481218	other
34828	4 9431269475	AA292436	Homo sapiens semaphorin F homolog mRNA complete cds	SS, TM
14985	4.941621032	U15128	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds	?
18115	4.5377553522	AA004420	ESTs	?
42506	4.9348587118	W70074	EST	other
34761	4 9316837445	AA287833	ESTs	other
11870	4 9281056201	AA262587	ESTs	TM
23211	4 9256391854	T40889	ESTs	other
40611	4.9160507275	N39138	Homo sapiens mRNA for KIAA0584 protein partial cds	other
42611	4 9128605354	W87006	Homo sapiens putative RNA binding protein KOC (koc) mRNA complete cds	other
39652	4 9045174605	H03099	ESTs	other
17581	4.889674751	AA129395	EST	?
37239	4.8704375369	AA449121	ESTs	?
18712	4 8703618781	F04677	ESTs	other
30709	4.8611171953	N51752	ESTs Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]	other
34179	4.8503613948	AA227903	ESTs Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]	other
21433	4.825670988	R22183	EST	?
39731	4.8186142741	H11760	ESTs	other
31295	4.8116814607	N86653	ESTs	other
24647	4.804163055	Z38108	EST	?
31292	4.8008871817	N66615	ESTs	other
1285	4.7997542393	HG4157-HT4427	EST - HG4157-HT4427	?
1106	4 7932425858	HG2981-HT3127	EST - HG2981-HT3127	?
18212	4.7912282565	AA196506	ESTs	other
34367	4.782207045	AA251758	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA complete cds	other
34802	4.7797760205	AA291468	ESTs	TM
34702	4.7775301546	AA287834	ESTs	other
11595	4.7696612848	AA242819	ESTs	other
8295	4.7639839111	AA405082	ESTs	?
17622	4.758635576	AA131584	ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]	other
35781	4.7572463523	AA406335	ESTs	other
34754	4.7483874972	AA287642	Human mRNA for KIAA0078 gene complete cds	other
23237	4.7444854356	T47281	EST	?
37667	4.7280445357	AA460318	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L26 [Rattus norvegicus]	other
11568	4.7257189975	AA236786	ESTs	other
38622	4.7190895733	AA598967	ESTs	?
5137	4.7057359474	U79296	Dihydroisopropylidene S-acyltransferase (E2 component of pyruvate dehydrogenase complex)	other
25038	4.7002244728	AA010065	CDC28 protein kinase 2	other
19288	4.7000147312	H16567	ESTs	other
32503	4.6979488292	T17045	Collagen type I alpha-2	other
3278	4.6953739298	M94055	SODIUM CHANNEL PROTEIN BRAIN II ALPHA SUBUNIT	TM
9696	4.6942081018	L38961	Integral transmembrane protein 1	TM
35400	4.6901390898	AA399591	Homo sapiens putative DNA methyltransferase (DNMT2) mRNA complete cds	other
35246	4.6862691303	AA398367	EST Weakly similar to HSP60 protein [M.musculus]	?
36387	4.6822499271	AA428270	ESTs	other
21509	4.6730072542	R27314	ESTs	other
31381	4.6729672124	N67889	ESTs	other
26723	4.6727894925	AA282781	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP28 [Saccharomyces cerevisiae]	other

FIGURE 8 (cont.)

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36326	4.6703621086	AA425151	Human GAP SH3 binding protein mRNA complete cds	other
17409	4.6658418667	AA113136	EST - RC_AA113136	other
4908	4.6552339935	U67156	Human mitogen-activated kinase kinase kinase 5 (MAPKKK5) mRNA complete cds	other
30594	4.6496238328	N49967	ESTs	other
38286	4.64639735	AA489847	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Nycotaceae coucang]	?
13073	4.6426509459	AA433950	ESTs	other
40435	4.6240181066	N21614	Homo sapiens basic-leucine zipper transcription factor MafG (MAFG) mRNA complete cds	other
14474	4.6228594379	AA609427	ESTs Moderately similar to III ALU SUBFAMILY 5C WARNING ENTRY III [H.sapiens]	other
38213	4.615309907	AA488847	ESTs Weakly similar to putative p150 [H.sapiens]	?
5312	4.606644198	U90716	Human cell surface protein HCAR mRNA complete cds	SS, TM
24225	4.6041550359	W70326	ESTs	?
35588	4.5868982366	AA401750	EST	?
29739	4.5863199051	H99628	EST	?
7203	4.5792992577	AA053096	EST - AA053096	other
2157	4.5772055869	L41839	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds	SS, TM
32066	4.5661024279	R11510	ESTs	?
8065	4.5648114738	AA314779	ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]	SS
224	4.5622018989	D13633	Human mRNA for KIAA0008 gene complete cds	other
34008	4.5609980241	AA188761	DNA polymerase gamma	other
33656	4.5557384389	W85477	ESTs	other
34065	4.5537335124	AA195517	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	TM
6028	4.5357922097	X68503	Adenylosuccinate synthase	other
4186	4.5032930671	U29463	Cytochrome B561	?
40262	4.5024727522	H93562	ESTs	TM
22687	4.5018672549	R88209	ESTs	TM
41069	4.4977510482	H93969	H.sapiens mRNA for hFat protein	SS
8264	4.4793100575	AA401334	ESTs	other
27588	4.472017297	AA443187	ESTs	other
35882	4.4717597552	AA412047	ESTs	?
34479	4.465519191	AA262080	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	TM
15921	4.4548516436	Y12065	Homo sapiens mRNA for nucleolar protein hNop56	?
11279	4.4380038671	AA195399	ESTs	other
39222	4.4367650786	AA621348	ESTs Highly similar to DOLICHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE [Saccharomyces cerevisiae]	other
34428	4.4364736768	AA258526	ESTs	other
8771	4.432067373	AA491188	ESTs	other
22193	4.4189610024	R53891	Homo sapiens mRNA from chromosome 5q21-22 clone: A3-A	other
7698	4.4066170674	AA263032	ESTs	other
19902	4.3866145805	H66736	ESTs	other
9276	4.3868095209	D82374	ESTs	other
10716	4.3794529068	AA053319	ESTs	TM
13193	4.3751913512	AA442763	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]	other
5690	4.3723059417	X17820	NUCLEOSIDE DIPHOSPHATE KINASE A	other
35102	4.37147138	AA371509	EST - RC_AA371509	TM
17983	4.3612985467	AA169226	ESTs	other
24962	4.3497206925	AFFX-HUMTFRRM115_07	AFFX-HUMTFRRM11507_5	?
31680	4.3418539669	N74438	ESTs	other
27168	4.330306894	AA410258	ESTs	other
28731	4.3231846659	D20981	EST	?
28348	4.3212284908	AA608752	ESTs	other

FIGURE 8 (cont.)

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16335	4 3019961487	AA018587	ESTs Weakly similar to !!! ALU SUBFAMILY SP WARNING ENTRY !!! [H.sapiens]	?
33036	4 2915644973	W48580	ESTs Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]	other
30180	4 2697721925	N33144	ESTs	other
35591	4 2895541242	AA401758	ESTs Weakly similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]	SS,
25340	4 2721717135	AA054554	EST	?
28106	4 2659103748	AA485084	ESTs	other
38690	4 2649184307	AA600121	ESTs	other
20203	4 2626499431	N26855	ESTs Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]	other
10251	4 2608760694	R76185	ESTs Weakly similar to C01H6.7 [C.elegans]	SS,
12684	4 2604192389	AA417558	ESTs	SS,
31636	4 2509469427	N73680	Natural resistance-associated macrophage protein 2	TM
20769	4 2479765348	N67277	ESTs	other
1572	4 2353281083	K01884	EST - K01884	?
10923	4 2292322072	AA116036	ESTs	other
34380	4 2283782392	AA252414	ESTs	other
10132	4 2222816115	R35733	EST - R35733	other
16629	4 2161752119	AA036811	ESTs	other
25146	4 1969683794	AA026356	ESTs	?
28730	4 1965943098	D20959	ESTs Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]	other
10200	4 1874912391	R64521	ESTs	other
38695	4 1545794663	AA600176	ESTs	other
31365	4 150549979	N87550	ESTs	other
42379	4 1496120668	W37999	ESTs	other
28050	4 1428703354	AA479139	Acid phosphatase 1 soluble	other
2620	4 1386565707	M29474	Human recombination activating protein (RAG-1) gene complete cds	?
8927	4 1340593744	AF008442	Homo sapiens RNA polymerase I subunit hRPA39 mRNA complete cds	other
13379	4 1269549188	AA449741	ESTs Weakly similar to AF-9 PROTEIN [H.sapiens]	other
5134	4 1218251808	U79293	Human clone 23948 mRNA sequence	other
2628	4 1213948	M26581	Zinc finger protein 8 (clone HF.18)	other
38005	4 1160483666	AA479969	ESTs	other
36575	4 1127196584	AA431085	EST	?
18296	4 1121837207	AA213620	ESTs Weakly similar to putative p150 [H.sapiens]	?
29531	4 1111459313	H88853	EST - RC_H88853	TM
143	4 1095880506	AFFX- HUMTFRRM115 07	AFFX-HUMTFRRM11207_5	?
10970	4 0967613396	AA129390	ESTs	other
25636	4 0952825397	AA152305	Interferon (gamma)-induced cell line protein 10 from	SS,
19735	4 0937827853	H53038	EST	?
40711	4 0909709431	N53564	ESTs	other
4149	4 0901471427	U28386	RAG (recombination activating gene) cohort 1	TM
5767	4 0862784557	X53793	MULTIFUNCTIONAL PROTEIN ADE2	other
5503	4 0861035825	X05232	Stromelysin	SS,
20310	4 0641711656	N34893	ESTs Highly similar to HYPOTHETICAL 47.8 KO PROTEIN B0280.9 IN CHROMOSOME III [Caenorhabditis elegans]	other
458	4 0599824566	D38145	Prostaglandin I2 (prostaglandin) synthase	SS,
7814	4 0559685576	AA248406	ESTs	other
40230	4 0447282719	H90181	ESTs	SS,
33651	4 039204804	W95409	ESTs	other
16777	4 0231857929	AA046968	EST	?
19110	4 0094905222	H06778	ESTs	other
34442	4 0077010365	AA258093	HKR-T1	other
5099	4 004992433	U79247	Human clone 23599 mRNA sequence	TM

FIGURE 8 (cont.)  
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6209	3.9990473163	AA384220	ESTs	other
24408	3.9976585074	V90146	ESTs	other
26596	3.9974919787	AA279943	ESTs	other
16485	3.9811264008	AA026269	Spleen focus forming virus (SFFV) proviral integration oncogene sp1	other
32969	3.9804901745	V42451	ESTs	TM
27006	3.9799768093	AA396695	ESTs Weakly similar to E04F6.2 gene product [C.elegans]	other
29809	3.9528765967	N21043	EST	?
9596	3.9440163451	H91564	ESTs	TM
29024	3.9377633938	F09315	Homo sapiens mRNA for KIAA0563 protein partial cds	other
21694	3.9356365584	R39317	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds	other
13207	3.9299981104	AA443321	ESTs	other
37865	3.9143752629	AA476623	ESTs Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe]	other
36201	3.9129828172	AA421164	ESTs	?
6961	3.8981160269	AFFX-HUMTFRM11507_3	AFFX-HUMTFRM11507_3	?
17444	3.8927133817	AA115933	ESTs	other
25669	3.8919834527	AA157267	ESTs Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III [Caenorhabditis elegans]	TM
24862	3.89042252	Z41415	ESTs Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]	other
26685	3.889363206	AA281850	ESTs	?
42300	3.8850230366	T95850	ESTs	?
6495	3.8830844863	X92715	Zinc finger protein 74 (Cox52)	other
38804	3.8828045942	AA598803	ESTs	TM
36358	3.8826713718	AA425756	ESTs	other
30560	3.873276445	N49284	MYB PROTO-ONCOGENE PROTEIN	other
14413	3.8724468158	AA600150	ESTs	other
73823	3.8574824067	T91805	Homo sapiens mRNA for ST1C2 complete cds	other
36158	3.853096838	AA487021	EST	?
2572	3.8519747554	M27281	Vascular endothelial growth factor	other
40100	3.8464168967	H75933	Laminin receptor (2H5 epitope)	other
40258	3.8462992993	H93340	ESTs	TM
20944	3.8461621525	N74443	ESTs	other
20411	3.8459400966	N48963	Homo sapiens mRNA for KIAA0689 protein partial cds	other
10345	3.8457714481	AA001663	ESTs	other
31261	3.8451974374	N66248	EST	other
8513	3.8378410994	AA446990	ESTs	other
13877	3.8363409835	AA476604	ESTs	other
40748	3.8253562321	N56879	EST	?
14509	3.8152852193	AA609643	ESTs	other
10281	3.8065567331	R80333	ESTs	other
25284	3.8044158642	AA045074	ESTs Weakly similar to S2+D SS-A/Ro autoantigen [H.sapiens]	other
6730	3.7900025129	Y09305	H.sapiens mRNA for protein kinase Dyrk4 partial	other
16033	3.7884592402	AFFX-HUMISGF3A/M97935_MB	AFFX-HUMISGF3A/M97935_MB	?
39242	3.7827184808	AA621523	ESTs	other
27354	3.7794760435	AA425221	ESTs	?
4552	3.777263605	U49188	Human placenta (D#733) mRNA complete cds	SS, TM
18345	3.7756199108	AA227219	Homo sapiens CAGF9 mRNA partial cds	other
16754	3.7677416053	AA046067	EST - RC_AA046067	other
12752	3.7671137403	AA421250	ESTs	other
42463	3.7601033108	V60180	ESTs	other

FIGURE 8 (cont.)

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10614	3 7581669016	AA037357	ESTs	?
867	3 7458337989	D87716	Human mRNA for KIAA0007 gene partial cds	other
7608	3 7336047135	AA180967	ESTs	other
31795	3 732738742	N80703	ESTs	other
35377	3 7273784803	AA399453	EST - RC_AA399453	?
22828	3 7243928524	R98192	ESTs	other
25240	3 7243198336	AA039713	ESTs	other
11008	3 7197361366	AA134289	ESTs Weakly similar to ASH1 [D.melanogaster]	?
4341	3 7162349944	U38545	Human ARF-activated phosphatidylcholine-specific phospholipase D1a (hPLD1) mRNA complete cds	other
28833	3 7147818393	D59787	EST - RC_D59787_f	?
3750	3 7121007154	U09279	Collagen type XIX alpha 1	SS,
17483	3 6943413512	AA122147	ESTs	TM
16854	3 6915209471	AA055552	ESTs Weakly similar to KIAA0319 [H.sapiens]	TM
3709	3 6891656771	U07550	Heat shock 10 kD protein 1 (chaperonin 10)	other
1808	3 6652978422	L00205	KERATIN TYPE II CYTOSKELETAL 6D	?
24577	3 6617721053	Z38727	Homo sapiens mRNA for KIAA0555 protein complete cds	TM
31032	3 6570916388	N62508	ESTs	other
4951	3 6538195433	U69546	Human RNA binding protein Etr-3 mRNA complete cds	other
37660	3 6523275307	AA460225	ESTs	other
20418	3 6485357091	N49209	ESTs	other
27895	3 6485167436	AA470155	Homo sapiens coatomer protein (COPA) mRNA complete cds	?
7971	3 6434397185	AA287423	ESTs	other
27606	3 64303453	AA443793	ESTs	other
24877	3 6427250633	Z39338	ESTs Highly similar to POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR [Mus musculus]	other
11070	3 6406198277	AA148521	ESTs Weakly similar to putative p150 [H.sapiens]	TM
9328	3 6356048599	D89618	Homo sapiens importin-alpha homolog (SRP1gamma) mRNA complete cds	other
36826	3 634689802	AA435998	ESTs	other
17678	3 6300045795	AA134275	Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3	other
36209	3 6274694477	AA421266	ESTs Weakly similar to LIS-1 protein [H.sapiens]	other
34120	3 6258090412	AA211615	EST	?
38152	3 6248442011	AA486737	H.sapiens mRNA for 6m protein F	TM
38483	3 6184693268	AA504491	ESTs Weakly similar to contains similarity to C3HC4-class zinc finger [C.elegans]	TM
20064	3 6183699978	H98653	ESTs	TM
31256	3 5992620732	N68162	EST	?
9713	3 5985228843	L44338	Homo sapiens mRNA for KIAA0525 protein partial cds	other
28622	3 5786056147	D11837	ESTs	?
38057	3 5738105703	AA481549	EST - RC_AA481549	other
28763	3 5688723791	D45568	EST	?
16996	3 5680705709	AA069038	EST - RC_AA069038	TM
28628	3 5604144617	D11888	ESTs Moderately similar to PROHIBITIN [H.sapiens]	?
25804	3 5442954572	AA148885	ESTs	?
2492	3 5423964239	M22898	Tumor protein p53 (Li-Fraumeni syndrome)	?
14904	3 5411970737	T83389	ESTs Highly similar to GEPHYRIN [Rattus norvegicus]	other
25265	3 5347588502	AA043785	H.sapiens RY-1 mRNA for putative nucleic acid binding protein	other
13606	3 5327912417	AA456437	ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT [H.sapiens]	other
42307	3 5318436465	T96595	EST - RC_T96595	TM
1544	3 526202414	J05068	TRANSCOBALAMIN I PRECURSOR	SS,
42339	3 5195061035	VQ0272	ESTs Weakly similar to No definition line found [C.elegans]	other
42311	3 5183719631	T97257	ESTs	other
2023	3 5040279423	L34600	INITIATION FACTOR IF-2 MITOCHONDRIAL PRECURSOR	other

FIGURE 8 (cont.)

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4540	3 4955308569	U48807	Human MAP kinase phosphatase (MKP-2) mRNA complete cds	other
33707	3 4888534277	Z39297	Neuronal pentraxin II	other
17220	3 4755763461	AA083070	EST - RC_AA083070_s	SS,
24332	3 4725273806	W85782	ESTs	other
35867	3 4668063718	AA412067	ESTs	other
20158	3 4538150055	N23638	ESTs Weakly similar to coded for by C. elegans cDNA y452e10.5 [C. elegans]	other
8338	3 4465832071	AA417152	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds	other
387	3 4421827234	D28589	EST - D28589	other
12319	3 4356289717	AA398109	ESTs	SS,TM
38278	3 4313139432	AA489711	ESTs	TM
15643	3 4312184246	W58247	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]	other
11218	3 4232932843	AA180488	ESTs	TM
16539	3 417686379	AA029328	Human mRNA for KIAA0073 gene partial cds	?
28203	3 4162847487	H28581	ESTs	other
13838	3 4182403464	AA465342	ESTs	other
25585	3 4160353003	AA112389	H4(D10S170)	SS,
34018	3 4145338583	AA191488	Human high-affinity copper uptake protein (hCTR1) mRNA complete cds	TM
251	3 4006042651	D14520	Basic transcription element binding protein 2	other
3778	3 4004518201	U09849	Zinc finger protein 139 (clone pHZ-37)	other
24535	3 3964397637	Z38408	ESTs	other
18858	3 3925184041	AA055759	Human mRNA for KIAA0128 gene partial cds	TM
18127	3 3921845927	AA004669	ESTs	other
36683	3 3841316491	AA432288	ESTs	other
26149	3 3809497785	AA250824	ESTs Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]	other
4011	3 3798089471	U20530	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA complete cds	other
41001	3 3794250205	N78844	ESTs	other
5660	3 3789336731	X16396	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE	SS,
19204	3 3778332343	H11829	ESTs	other
42323	3 3768515979	T98152	Fibrin 2	SS,
26828	3 3725378868	AA342580	ESTs	SS,
20497	3 3692858912	H52565	ESTs	other
19226	3 36674249	H12455	ESTs	other
36267	3 3606641838	AA424046	ESTs	other
32257	3 3559796018	R54726	DNA-REPAIR PROTEIN XRCC1	other
17365	3 3522214732	AA101551	ESTs	other
15296	3 3491193196	W16684	ESTs Moderately similar to Similar to S. cerevisiae hypothetical protein L3111 [H.sapiens]	other
17875	3 3485870272	AA134064	ESTs	TM
40332	3 3458469589	H97565	Homo sapiens mRNA from chromosome Sq21-22 clone A3-A	other
7219	3 3385684843	AA056319	Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA complete cds	other
10006	3 3322827922	H81183	Homo sapiens mRNA for KIAA0628 protein complete cds	?
33985	3 3276877441	AA181580	Homo sapiens importin beta subunit mRNA complete cds	other
9570	3 3263855302	H85168	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene complete cds	other
37551	3 3155406577	AA456679	ESTs	other
886	3 3111782759	D88613	Human mRNA for hGCMs complete cds	other
23650	3 3069426629	T86293	ESTs	other
18367	3 3007433533	AA224180	ESTs Moderately similar to ovarian-specific protein [R.norvegicus]	?
42494	3 2908070546	V89385	H.sapiens NuMA gene (Clone T33)	other
14310	3 2753564661	AA598412	ESTs Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION [Saccharomyces cerevisiae]	SS,TM

FIGURE 8 (cont.)

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19233	3.274416299	H12634	ESTs	other
42263	3.2731086284	T94343	Homo sapiens M962 protein spliced isoform 2 mRNA complete cds	other
12809	3.271352097	AA424406	ESTs	other
36265	3.2696023617	AA424489	ESTs	other
21555	3.2666296446	R33073	EST	?
13767	3.2665695616	AA463234	ESTs	TM
4739	3.2661561937	U58766	Human FX protein mRNA complete cds	other
7258	3.263106866	AA075427	ESTs	other
17041	3.2629042078	AA070384	EST - RC_AA070384	?
15504	3.2616745245	W28362	ESTs	other
23793	3.2611829896	T90971	EST - RC_T90971	other
18214	3.2572346955	AA196635	ESTs	TM
7401	3.257164123	AA094800	Human translation initiation factor eIF3 p66 subunit mRNA complete cds	other
18912	3.2553600001	F10913	Homo sapiens clone 23617 unknown mRNA partial cds	other
36317	3.2509495347	AA425069	Human mRNA for KIAA0334 gene complete cds	?
9410	3.2507279851	H20443	H.sapiens mRNA for TRES	other
2146	3.2464307896	L41390	EST - L41390	?
18683	3.240814335	F04258	ESTs Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]	?
33891	3.2392191408	AFFX-HUMTFRRM11507_M	AFFX-HUMTFRRM11507_M	?
14435	3.2372161315	AA608730	ESTs Weakly similar to ELONGATION FACTOR 1-ALPHA (Giardia intestinalis)	other
9584	3.2363829855	H88126	ESTs Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]	other
22081	3.2340096572	R49218	ESTs	TM
35796	3.233287605	AA410223	EST - RC_AA410223	?
37403	3.2261852043	AA453613	ESTs	other
15796	3.2260359988	X16889	ALPHA-GALACTOSIDASE A PRECURSOR	SS.
15840	3.2257932439	X70944	PTB-ASSOCIATED SPLICING FACTOR	other
7518	3.2252170427	AA147144	EST - AA147144	other
32335	3.2228388982	R76248	ESTs	other
3256	3.2180538038	M92439	130 KD LEUCINE-RICH PROTEIN	other
4400	3.2173896081	U41387	Human Gu protein mRNA partial cds	other
7681	3.2074414299	AA206983	Homo sapiens mRNA for DRM protein	other
15676	3.2041299443	W69849	ESTs	TM
39590	3.2038953621	F09281	ESTs	other
26883	3.1980022253	AA291921	ESTs Weakly similar to putative p150 [H.sapiens]	?
9808	3.1920380384	M80627	Transcription factor 12 (HTF4 helix-loop-helix transcription factors 4)	other
27755	3.1900699454	AA453444	ESTs	other
29983	3.1882280623	N26011	ESTs	?
21350	3.1876957756	R15846	ESTs	other
11981	3.1870525747	AA280928	ESTs	other
23930	3.1817500097	T96690	ESTs Weakly similar to IIR ALU SUBFAMILY J WARNING ENTRY!!!! [H.sapiens]	other
30399	3.1792054412	N45226	EST	?
22786	3.1781990049	R58312	ESTs	other
13494	3.1673900969	AA453431	ESTs	TM
12908	3.1530533441	AA427579	ESTs	other
22319	3.1469419301	R60567	ESTs	TM
31309	3.1466750623	N66818	ESTs	TM
31192	3.1458778823	N64406	ESTs	other
11288	3.144833134	AA196512	ESTs	TM
170	3.1430726349	D00596	Thymidylate synthase	?
5307	3.1347905628	U90549	Human non-histone chromosomal protein (NHIC) mRNA complete cds	other

FIGURE 8 (cont.)

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26105	31311103325	AA243133	Homo sapiens serine/threonine kinase (STAK) mRNA complete cds	other
11659	31281785108	AA251909	Homo sapiens MAD3-like protein kinase mRNA complete cds	other
19177	3124408565	H10984	ESTs	TM
8389	31241545824	AA425230	ESTs	TM
34087	31216555797	AA205125	Protein serine/threonine kinase s62	other
25001	31209327466	AA004718	ESTs Weakly similar to BAP31 protein [H.sapiens]	other
14149	31198500308	AA489665	ESTs	other
10167	31191966923	R55076	ESTs	other
17380	31071055868	AA102566	ESTs	other
42397	31044680628	W42928	ESTs	other
14935	31042015743	T84828	ESTs Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]	other
41673	31030349819	R78618	ESTs Weakly similar to GTP-binding protein rab10 [R.nonvegicus]	other
2750	31026223619	M35999	Integrin beta 3 (platelet glycoprotein IIs antigen CD61)	?
3190	31026223619	M86808	PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT TESTIS-SPECIFIC FORM PRECURSOR	?
17406	3099394188	AA112979	Homo sapiens mRNA for VRK1 complete cds	other
598	30912414004	D59253	Homo sapiens mRNA for low molecular mass ubiquitinone-binding protein complete cds	other
29348	30802365759	H69021	ESTs	other
14130	30744457534	AA489041	ESTs	other
14134	3069660341	AA489080	ESTs Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]	other
42421	30684159011	W45491	ESTs Weakly similar to T23G11.7 [C.elegans]	other
15723	30660746209	W79060	ESTs Highly similar to ribosome-binding protein p34 [R.nonvegicus]	other
11140	30650815188	AA158132	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae]	other
28531	30649767987	C20679	ESTs	other
2021	30628707497	L34409	Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA fragment	?
14522	3058260163	AA610108	ESTs Highly similar to PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C21E11.05C [Schizosaccharomyces pombe]	SS
28853	30545821815	N22182	ESTs	other
15962	30521475703	Z21420	ESTs	other
6541	30508060038	X95632	Human Abi interactor 2 (Abi-2) mRNA complete cds	other
13229	30485366337	AA443811	ESTs	other
27315	3046822812	AA424038	ESTs	other
13521	30302305369	AA456821	ESTs Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]	other
35929	30269182409	AA412429	ESTs	other
17925	30253428426	AA164209	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds	other
5053	30249536782	U76992	Human Tat-SF1 mRNA complete cds	other
15060	30213293848	U54999	Human LGN protein mRNA complete cds	other
17757	30205801351	AA147224	EST	?
19050	30192379314	M05509	ESTs	other
26530	30179823278	AA278650	ESTs	other
16806	30158779932	AA053258	Homo sapiens mRNA for KIAA0648 protein partial cds	TM
29088	30149440394	F13700	Homo sapiens ribonuclease P protein subunit p40 (RPP40) gene complete cds	other
22960	30141662421	T10272	ESTs	other
33585	30121872451	W93000	ESTs	other
220	30109180714	D13627	Human mRNA for KIAA0002 gene complete cds	TM
4288	30024671054	U36448	Human Ca2+-dependent activator protein for secretion mRNA complete cds	TM
7445	29995643641	AA104023	ESTs	?
40903	29990347068	N68670	ESTs	?
18055	29973386648	AA179387	ESTs	other
7282	29962782596	AA083339	ESTs	other

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9348	2.9949017671	H03686	ESTs	TM
806	2.9877476515	D87009	Human (lambda) DNA for immunoglobulin light chain	?
38447	2.9876031644	AA504255	Human protein kinase ATR mRNA complete cds	other
41464	2.9870604981	R46837	ESTs	?
9662	2.9869252306	L19161	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT	other
16976	2.9801154057	AA063625	EST	?
37426	2.9756408909	AA454016	ESTs	other
2568	2.9725898298	M27878	Zinc finger protein 84 (HPF2)	other
15174	2.9695024379	U82987	Human Bcl-2 binding component 3 (bbc3) mRNA partial cds	other
33620	2.9657446567	V693943	ESTs	other
6784	2.9655061112	Y11681	Homo sapiens ribosomal protein S12 gene nuclear gene encoding mitochondrial protein complete cds	?
41077	2.9642389716	N95026	ESTs	TM
1932	2.9609985996	L24804	Human (p23) mRNA complete cds	other
32556	2.9586984022	F03738	ESTs	other
16106	2.9574232912	AA002256	ESTs	SS
32156	2.9574232912	R40381	ESTs	?
13617	2.9552305838	AA456646	ESTs	other
11889	2.9552039991	AA281251	ESTs Weakly similar to trithorax protein trill [D.melanogaster]	other
6056	2.9476541132	X68194	Pantophysin (human keratinocyte line HaCat mRNA 2106 nt)	TM
15446	2.9445456286	V627374	Homo sapiens 10kD protein (BC10) mRNA complete cds	other
38086	2.9445277634	AA482557	EST	?
13878	2.9444133384	AA478604	ESTs	other
6209	2.9422425032	X76770	H.sapiens PAP mRNA	other
388	2.9357591919	D28791	Phosphatidylinositol glycan class A (paroxysmal nocturnal hemoglobinuria)	?
1351	2.9266145582	HG4755-HT5203	EST - HG4755-HT5203	?
42824	2.9266145582	V87804	ESTs	other
34895	2.9242794509	AA311972	ESTs	other
20157	2.9214162976	N23393	ESTs	other
29248	2.9188102156	H52918	ESTs	?
4893	2.9178533564	U66615	Human SWI/SNF complex 155 KDa subunit (BAF155) mRNA complete cds	other
10104	2.9150324884	R23655	ESTs	TM
15039	2.9147218324	U46116	Protein tyrosine phosphatase receptor type gamma polypeptide	?
1605	2.9141775797	L00058	V-myc avian myelocytomatosis viral oncogene homolog	?
4536	2.907660336	U48705	Receptor protein-tyrosine kinase EDDR1	?
10173	2.905710598	R56678	ESTs Weakly similar to cell division control protein CDC21 [H.sapiens]	?
26555	2.9056210172	AA278071	ESTs Weakly similar to T08A11.2 [C.elegans]	other
4401	2.9047655582	U41515	Human deleted in split hand/split foot 1 (DSS1) mRNA complete cds	other
21009	2.8995011918	N90401	ESTs	TM
3602	2.894817322	U01317	HEMOGLOBIN EPSILON CHAIN	?
4833	2.8919254016	U63455	Sulfonylurea receptor (hyperinsulinemia)	?
36200	2.8912301426	AA421164	ESTs	?
26845	2.8898309441	AA281076	ESTs	other
35299	2.8887661574	AA398622	Transcription factor 6-like 1 (mitochondrial transcription factor 1-like)	other
9804	2.8880347344	M74558	Human SIL mRNA complete cds	other
5216	2.8877977515	U83410	Human CUL-2 (cul-2) mRNA complete cds	other
12313	2.8847621603	AA397918	ESTs	other
5928	2.8836060438	X62048	WEE1-LIKE PROTEIN KINASE	?
39586	2.8818258313	F09155	ESTs	TM
34758	2.8775214637	AA287680	EST	?
16199	2.8753649024	AA195318	ESTs	other

FIGURE 8 (cont.)

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18667	2.8720874689	H61476	ESTs	?
6081	2.8679372936	X69398	CD47 antigen (Rb-related antigen integrin-associated signal transducer)	SS, TM
5254	2.862087239	U86782	Human 26S proteasome-associated pad1 homolog (PDH1) mRNA complete cds	other
13578	2.8570820484	AA455967	Human neuronal PAS2 (NPAS2) mRNA complete cds	?
1117	2.8568053461	HG3075-HT3236	EST - HG3075-HT3236	?
20533	2.8564678641	N54407	ESTs	TM
38495	2.8562453397	AA505118	Human nucleoporin 98 (NUP98) mRNA complete cds	other
33728	2.8548155651	Z39654	EST	?
2028	2.8532778139	L35035	RIBOSE 5-PHOSPHATE ISOMERASE	other
27374	2.8520674335	AA425816	ESTs Weakly similar to Y53C12A.3 [C.elegans]	other
19404	2.8518690748	H20568	ESTs	other
26108	2.8504706329	AA243189	ESTs	SS,
4189	2.8439972255	U30930	UDP glycosyltransferase 6 (UDP-galactose ceramide galactosyltransferase)	TM
16708	2.8427388072	AA043944	ESTs	other
357	2.8350474214	D26156	Human mRNA for transcriptional activator hSNF2b complete cds	other
26045	2.8315740098	AA238276	ESTs	other
17796	2.8312342777	AA150435	ESTs	other
6059	2.8288722809	AA310967	ESTs Weakly similar to T04A8.11 [C.elegans]	other
40914	2.827999584	N69220	ESTs	other
27169	2.8263163852	AA410287	H.sapiens mRNA for basic transcription factor 2.34 kD subunit	other
21358	2.8262413945	R16078	ESTs	other
3572	2.8261469131	S87759	Protein phosphatase 2C alpha (human teratocarcinoma mRNA 2346 nt)	other
11877	2.8259099942	AA262727	ESTs	other
1653	2.8234017508	L05424	CD44 antigen (cell adhesion molecule)	?
24645	2.8131264428	Z39106	ESTs	other
35830	2.8128257031	AA411448	ESTs	TM
4433	2.8114422177	U43279	EST - U43279	?
20151	2.8109454503	N22895	Homo sapiens clone 1400 unknown protein mRNA partial cds	other
38648	2.8084431065	AA599267	EST - RC_AA599267	other
7777	2.8071817829	AA236870	ESTs	other
32845	2.80583194	V031566	EST	?
28258	2.8043934182	AA505133	ESTs	other
6853	2.798263202	Z22951	TRANSCRIPTION FACTOR PG5	?
35944	2.7913872996	AA412488	ESTs	?
30648	2.7866523876	N50871	ESTs	?
18965	2.7857482775	H01411	ESTs	TM
8618	2.785444221	AA460077	ESTs	other
14945	2.7838257917	T99606	ESTs Weakly similar to F35G2.2 [C.elegans]	other
8375	2.7805657722	AA422160	H.sapiens NAP (nucleosome assembly protein) mRNA complete cds	other
34929	2.7792111121	AA342084	EST - RC_AA342084	other
328	2.7766978435	D21262	Human mRNA for KIAA0035 gene partial cds	other
27057	2.7761218063	AA400998	ESTs	SS,
36292	2.7748002184	AA424513	EST - RC_AA424513	other
6480	2.7735431318	X91788	H.sapiens mRNA for Ichi protein	other
15424	2.7731675808	V027054	APOLIPOPROTEIN AI REGULATORY PROTEIN-1	other
11602	2.7730818255	AA243007	ESTs	?
18175	2.77056688	AA194730	ESTs	?
25202	2.7696585896	AA034527	EST	?
1681	2.7697545972	L07493	Replication protein A (E coli RecA homolog RAD51 homolog)	other
14568	2.767984858	AA621122	ESTs	other
25814	2.7633374335	AA115769	ESTs	other

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14182	2.7606048934	AA490885	ESTs	other
31599	2.7591187956	N72106	EST	other
18253	2.7471964061	AA208370	ESTs	other
6193	2.7442487702	X76092	Regulatory factor (trans-acting) 3	other
22911	2.7433449659	T03865	ESTs	other
35545	2.743246906	AA401274	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds	other
35955	2.7389431758	AA412528	ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [R.norvegicus]	other
17642	2.7377607284	AA132983	ESTs Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [H.sapiens]	other
6131	2.7371784571	X72841	Human retinoblastoma-binding protein (RbAp46) mRNA complete cds	other
41429	2.7347564467	R44994	ESTs	other
17052	2.7323944181	AA070815	EST - RC_AA070815	other
34243	2.7294147034	AA235050	ESTs	?
22937	2.7284347248	T10065	Homo sapiens TLS-associated protein TASR-2 mRNA complete cds	other
5183	2.7243199196	U82130	Human tumor susceptibility protein (TSG101) mRNA complete cds	other
30837	2.7231409239	N54416	ESTs	other
16243	2.7228028265	AA012902	ESTs	TM
19954	2.7215183495	H80100	ESTs	other
6444	2.720441384	X89750	H.sapiens mRNA for TGF protein	other
5916	2.7192579481	X81072	Human mRNA for T cell receptor clone IGRA17	SS
6240	2.7168544194	X78627	H.sapiens mRNA for translin	?
42118	2.7144176166	T69924	EST - RC_T69924	other
7701	2.7107230468	AA215333	ESTs	TM
17568	2.7096978968	AA128905	ESTs	TM
42534	2.7086014274	W73189	Homo sapiens protein-tyrosine kinase EPHB2v (EPH82) mRNA complete cds	SS, TM
29813	2.708372123	N21111	ESTs	other
36898	2.7067394943	AA609458	ESTs	other
10316	2.7055636457	R88880	ESTs Moderately similar to zinc finger protein [M.musculus]	other
14769	2.7040621985	S54641	HZF-16	other
32961	2.7012196407	V38366	Human mRNA for KIAA0005 gene complete cds	other
35273	2.6975345483	AA388507	ESTs	other
10180	2.6960636303	R60100	ESTs	?
32563	2.6955462902	T27697	Human mRNA for KIAA0036 gene complete cds	other
34502	2.6948574449	AA262768	ESTs	TM
13223	2.6912995353	AA443720	ESTs	other
8494	2.6906516739	AA443460	ESTs	other
7776	2.6900717525	AA236771	ESTs	other
10400	2.6898958951	AA007234	ESTs	other
1130	2.6897527619	HG3132-HT3308	EST - HG3132-HT3308	?
2379	2.6874247447	M16937	Human homeo box c1 protein mRNA complete cds	TM
18906	2.6861450774	F10868	Human SH3 domain-containing protein SH3P18 mRNA complete cds	?
34795	2.6853510115	AA291259	ESTs	TM
41955	2.6821406177	T33311	Neuronal pentraxin II	other
2009	2.6791061739	L33881	Protein kinase C iota	?
33688	2.6775081286	Z38501	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 56]	other
1385	2.6771402807	HG884-HT884	EST - HG884-HT884	?
24758	2.6758060668	Z40075	ESTs	other
7620	2.6742248913	AA182464	ESTs Weakly similar to MITOCHONDRIAL INNER MEMBRANE PROTEASE SUBUNIT 2 [S.cerevisiae]	other
30733	2.6739544496	N52076	Homo sapiens mRNA for KIAA0637 protein complete cds	other
21256	2.6723253055	R09195	Homo sapiens mRNA for KIAA0584 protein partial cds	other
40528	2.669020458	N29325	ESTs Highly similar to 47 KD PROTEIN [Pseudomonas	other

FIGURE 8 (cont.)

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			chloroplast)	
25265	2.6685455406	AA045083	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE	other
9299	2.667949532	D82775	ESTs Weakly similar to unknown [S.cerevisiae]	SS.
12174	2.6669305328	AA292128	ESTs	other
38357	2.6652770538	AA491265	EST	TM
3154	2.6619596806	M83712	Cholinergic receptor nicotinic alpha polypeptide 5	TM
7383	2.655440738	AA093834	ESTs Weakly similar to HYPOTHETICAL 16.8 KD PROTEIN IN SMY2-RPS101 INTERGENIC REGION [S.cerevisiae]	other
1923	2.6530372325	L23808	Matrix metalloproteinase 12 (macrophage elastase)	SS.
24906	2.6527048053	Z41840	ESTs	other
34726	2.6495430564	AA287278	ESTs	SS.
30407	2.6495430564	N45883	ESTs	TM
20408	2.6459891347	N48787	ESTs Moderately similar to !!? ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]	other
7159	2.6455059455	AA037206	ESTs	TM
26286	2.6445106706	AA253351	ESTs	?
19822	2.6431968212	H58684	ESTs	?
12379	2.6428192941	AA399418	Homo sapiens mRNA for JM23 protein complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin))	other
22698	2.6396306055	R89287	ESTs	other
24161	2.6394502284	V58015	ESTs	other
9558	2.6370149706	H81497	ESTs	TM
18104	2.6358767288	AA188801	ESTs	other
24882	2.6357248889	Z41563	ESTs	other
40038	2.6347974784	H69485	ESTs	other
8865	2.6344645492	AB002359	Human mRNA for KIAA0361 gene KIAA0361 protein	other
22148	2.6288326966	R51831	ESTs	other
4627	2.6277060831	U51990	Human hPip18 mRNA complete cds	other
8394	2.6275394634	AA426156	ESTs	TM
20422	2.6272599716	N49300	ESTs	other
41602	2.6258613824	R67258	ESTs Moderately similar to rhotein [M.musculus]	other
812	2.6257836682	D63480	Human mRNA for KIAA0146 gene partial cds	TM
4821	2.619521444	U62801	Human protease M mRNA complete cds	SS, TM
16807	2.617722928	AA053296	ESTs	other
15288	2.6173997018	W07562	ESTs Moderately similar to rA8 [R.novgicus]	other
38023	2.6135617291	AA481066	ESTs	other
23822	2.6120077647	T91715	ESTs Highly similar to HYPOTHETICAL 103.6 KD PROTEIN IN COX5B-PFK26 INTERGENIC REGION [Saccharomyces cerevisiae]	TM
10951	2.6116018519	AA126719	ESTs	other
6150	2.6113980879	X74282	RETINOBLASTOMA BINDING PROTEIN P48	other
39336	2.6109987712	C20945	ESTs Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]	other
17793	2.6102158178	AA150242	ESTs Highly similar to modulator recognition factor 2 [H.sapiens]	other
26891	2.6085107387	AA292659	ESTs	other
2175	2.607468570	L42621	Homo sapiens Ly-9 mRNA complete cds	TM
10642	2.6048724507	AA040149	Human Chromosome 16 BAC clone C17987SK-A-270G1	other
15026	2.6031453592	U41816	Human C-1 mRNA complete cds	other
7699	2.6019047419	AA215299	Homo sapiens chromosome 19 cosmid R30783	other
8543	2.6011828937	X95654	Homo sapiens mRNA for SCP-1 complete cds	other
20036	2.5993684878	N82122	ESTs	other
11308	2.5993311375	AA207114	ESTs	other
4086	2.5966382866	U24704	Human endocrine factor-1 mRNA complete cds	other
38615	2.5963996726	AA598938	EST - RC_AA598938	other
11819	2.5951501969	AA258189	ESTs	other

FIGURE 8 (cont.)

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37433	2.5957446266	AA54103	ESTs	other
28270	2.5939657529	AA521186	ESTs	TM
5587	2.5932338399	X13482	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'	other
19841	2.5930132063	H59617	ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Drosophila melanogaster]	other
10655	2.5825442731	AA040882	ESTs	?
14053	2.5899324577	AA485147	ESTs Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R0SD3.2 IN CHROMOSOME III [Caenorhabditis elegans]	other
31574	2.5883094453	N71303	EST	?
7814	2.5870699315	AA187579	ESTs Weakly similar to Ye007c-ep [S.cerevisiae]	other
37971	2.5847445397	AA479185	EST	?
7090	2.5845365105	AA009913	Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds	other
17852	2.5841100415	AA156360	ESTs	other
24219	2.5823376094	W69960	ESTs	other
19070	2.5813645258	H05970	Human clone 23960 mRNA sequence	?
17719	2.5803608155	AA136569	EST	?
38569	2.579106781	AA599694	Human mRNA for KIAA0133 gene complete cds	TM
20982	2.5783957078	N79565	ESTs	TM
9158	2.5731838907	D31446	Homo sapiens breakpoint cluster region protein 1 (BCRG1) mRNA complete cds	other
11382	2.5731137778	AA227261	ESTs	other
8613	2.5723118482	AA459555	Homo sapiens mRNA for KIAA0648 protein partial cds	TM
13866	2.5715997844	AA476319	ESTs	SS,
10303	2.5712615907	R86178	Ataxia telangiectasia mutated (includes complementation groups A C and D)	?
22289	2.567916035	R59801	EST	?
18257	2.5673459608	AA206591	EST - RC_AA206591	other
20555	2.5654242568	N55168	ESTs	other
39552	2.5645918108	F03605	PUTATIVE 60S RIBOSOMAL PROTEIN	other
27530	2.5631130948	AA435999	ESTs	other
1795	2.5608471476	L13434	Human chromosome 3p21.1 gene sequence complete cds	?
14746	2.5603154966	D50354	Human mRNA for KIAA0007 gene partial cds	other
2993	2.5587815672	M64929	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform	other
19191	2.5545280975	H11297	ESTs	other
12889	2.5507999853	AA430032	ESTs Moderately similar to PTTG gene product [R.norvegicus]	?
15452	2.5488533884	W27451	Human Cdc5-related protein (PCDC5RP) mRNA complete cds	other
18003	2.5465671712	AA171692	ESTs	other
24198	2.5461854497	W67524	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence	TM
42653	2.5447526827	W92703	ESTs	other
26446	2.544106171	AA258796	EST Weakly similar to putative p150 [H.sapiens]	?
30438	2.5369548574	N47204	ESTs Weakly similar to C50F4.12 [C.elegans]	other
36365	2.5362912735	AA425893	ESTs Weakly similar to probable CBP3 protein homolog [C.elegans]	other
28135	2.535658968	AA243765	ESTs	other
41885	2.5349932888	T23449	ESTs Moderately similar to ZNF127-Xp [H.sapiens]	SS,
15457	2.5343495968	W27560	ESTs	other
27748	2.5320767519	AA453158	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds	other
32315	2.5302979959	R69840	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Nycticebus coucang]	?
25310	2.5274401579	AA046745	ESTs	other
42720	2.5222453766	Z39436	ESTs	other
12939	2.5200945911	AA428204	ESTs	other
30746	2.5198420998	N52243	ESTs	other
2222	2.5183624578	L76703	Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA complete cds	?
11609	2.5191785545	AA243303	ESTs	TM

FIGURE 8 (cont.)

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9658	2.5185814336	L16991	Deoxythymidylate kinase	other
12210	2.5172044681	AA293774	ESTs Weakly similar to PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE MITOCHONDRIAL [C.elegans]	other
3563	2.5169918533	S83364	EST - S83364	other
42407	2.5128230047	W44768	Homo sapiens nephrocystin (NPHP1) mRNA partial cds	?
32826	2.5128052161	W20391	Human mRNA for kinesin-related protein partial cds	other
9692	2.5119977116	L37747	LAMIN B1	?
27862	2.5094571267	AA458908	ESTs	TM
33691	2.509287494	Z39630	EST	other
17288	2.5088624644	AA065178	ESTs	SS
9888	2.5076170902	N35449	ESTs Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]	other
5932	2.5073880985	X82153	Minichromosome maintenance deficient (S. cerevisiae)	other
15885	2.5053862932	X95073	H.sapiens mRNA for transin associated protein X	other
17952	2.5049193223	AA185677	ESTs Weakly similar to F16A11.1 [C.elegans]	other
12197	2.5042458391	AA293206	ESTs	other
6210	2.5042034456	X76942	Homo sapiens golgin-245 mRNA complete cds	other
34047	2.5041917773	AA194166	ESTs Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens]	other
16929	2.5034461307	AA058952	ESTs	other
26834	2.5028075682	AA287138	ESTs Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus (Thermophilus)]	other
5157	2.5017270258	U80034	Human mitochondrial intermediate peptidase precursor (MIPEP) mRNA mitochondrial gene encoding mitochondrial protein complete cds	other
38434	2.5005880672	AA497013	ESTs	?
33269	2.5000262771	W72967	ESTs	other
26991	2.4990009911	AA398284	ESTs	other
7590	2.4948786183	AA173505	ESTs Weakly similar to HYPOTHETICAL 46.1 KD PROTEIN IN PHO2-POL3 INTERGENIC REGION [S.cerevisiae]	other
14960	2.4896232864	U05237	Human (fetal) Altz-50-reactive clone 1 (FAC1) mRNA complete cds	other
13585	2.4866752902	AA455999	ESTs Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]	other
35901	2.4847673158	AA412151	ESTs	other
38185	2.4826740426	AA487508	Homo sapiens mRNA for KIAA0658 protein complete cds	other
34678	2.4824371274	AA284744	Annexin XI (56kD autoantigen)	other
1424	2.4811113231	J02645	Eukaryotic translation initiation factor 2A	other
16778	2.4800522256	AA047008	ESTs	other
21876	2.4789005203	R43286	EST - RC_R43286	?
17779	2.4695725489	AA149641	ESTs	other
24559	2.4682754649	Z38588	ESTs	other
7781	2.467947166	AA242904	Homo sapiens proline-rich G1a protein 1 (PRGP1) mRNA complete cds	?
7474	2.4677129013	AA126592	ESTs Weakly similar to No definition line found [C.elegans]	other
34290	2.4675279697	AA236806	ESTs	other
5316	2.4673813483	U90905	Human clone 23574 mRNA sequence	TM
10218	2.4645666539	R68884	ESTs Highly similar to HYPOTHETICAL 44.2 KD PROTEIN IN SCO2-MRF1 INTERGENIC REGION [Saccharomyces cerevisiae]	other
18109	2.4634292267	AA188961	Homo sapiens retinoblastoma-associated protein HEC mRNA complete cds	?
6485	2.4613518897	X92096	H.sapiens mRNA for transmembrane protein mp24	SS, TM
34954	2.4591845976	AA342959	EST - RC_AA342959	?
42558	2.4588830205	W74751	ESTs	other
27444	2.4585750563	AA430180	ESTs Weakly similar to F25H9.7 [C.elegans]	other
21284	2.4582503599	R10301	EST	?
8920	2.4568596729	AF006265	Homo sapiens cancer associated surface antigen (RCAS1) mRNA complete cds	other
30037	2.4544484116	N27439	ESTs	TM
27602	2.4527990177	AA443702	ESTs Weakly similar to W02812.7 [C.elegans]	TM

FIGURE 8 (cont.)

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3390	2 4525517032	S59184	RYK receptor-like tyrosine kinase	TM
25040	2 452352841	AA010188	ESTs	other
37713	2 4487800271	AA461317	ESTs	other
40477	2 4477660739	N24005	Homo sapiens BAC clone RG300E22 from 7q21-q31.1	other
29382	2 4470532391	H72914	ESTs	other
35521	2 4465885349	AA400831	ESTs	other
20324	2 4464518504	N35406	Phospholipase C beta 4	SS
16620	2 4460334893	F02506	ESTs	other
21087	2 4406971835	R00186	EST	?
9950	2 4398530157	N71503	ESTs	other
31965	2 4363228422	N93629	ESTs	SS
15120	2 4345896403	U73524	Human putative ATP/GTP-binding protein (HEAB)	TM
28613	2 4339770686	D59257	Human C-1 mRNA complete cds	other
38082	2 4295434916	AA482284	ESTs	other
34723	2 428289395	AA267115	ESTs	other
7960	2 427332589	AA285277	Homo sapiens brain expressed ring finger protein mRNA complete cds	other
18073	2 4231728031	AA180453	EST	other
36755	2 4222443392	AA435698	EST - RC_AA435698	other
18927	2 4187841215	F11087	ESTs	other
3457	2 4186224787	S74728	Andiquin	TM
38606	2 4177693475	AA598844	ESTs	other
20967	2 41519947	N76086	ESTs	other
24752	2 4141438374	Z40012	Homo sapiens mRNA for KIAA0587 protein complete cds	other
28443	2 4138974256	AA621611	ESTs	?
452	2 4135942278	D38076	RAN binding protein 1	other
11701	2 4134095351	AA253031	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds	other
13655	2 412509306	AA458919	ESTs Weakly similar to 26S proteasome subunit p44.5 [H.sapiens]	other
24822	2 4119066031	Z40958	ESTs	other
12672	2 4112720798	AA417087	ESTs	other
4836	2 4106618618	U83717	Human osteoclast stimulating factor mRNA complete cds	other
42200	2 4083826789	T83729	EST - RC_T83729	?
10987	2 4078548868	AA132239	ESTs Highly similar to HYPOTHETICAL 47.4 KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]	other
35672	2 4073821434	AA404995	EST - RC_AA404995	other
6224	2 405310553	X77748	Glutamate receptor metabotropic 3	TM
28395	2 404213441	AA610064	ESTs	other
36390	2 4032664297	AA426291	ESTs Weakly similar to No definition line found [C.elegans]	other
21045	2 4031905687	N93403	ESTs	?
4558	2 4024665999	U48379	Human diacylglycerol kinase epsilon DGK mRNA complete cds	TM
12916	2 3998505067	AA427745	ESTs	other
20850	2 3998090334	N69514	ESTs Weakly similar to oxidoreductase [H.sapiens]	other
29759	2 3986103066	I199872	ESTs	other
36786	2 3971559161	AA435815	Human Cdk-associated Rb cyclophilin CARS-Cyp mRNA complete cds	other
31942	2 3947415736	N93185	ESTs	other
7097	2 39382714	AA011452	ESTs	other
39462	2 3936147708	D60063	ESTs	other
14420	2 3919915706	AA600322	ESTs Highly similar to AAC-RICH MRNA CLONE AAC3 PROTEIN [Dictyostelium discoideum]	other
34829	2 3916035475	AA282527	EST - RC_AA282527	other
27431	2 3905463084	AA428038	ESTs	TM
6387	2 3904071656	X85372	H.sapiens mRNA for Sm protein F	other
11342	2 3902176276	AA223874	Homo sapiens mRNA for KIAA0704 protein partial cds	other

FIGURE 8 (cont.)

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1497	2.368369765	J04068	Topoisomerase (DNA) II alpha (170kD)	other
9841	2.3541922016	M85724	Centromere autoantigen C	other
11454	2.3620201875	AA233854	ESTs	TM
29950	2.3807499489	N24902	Homo sapiens mRNA for E10-55kDa-associated protein	TM
8396	2.3807187289	AA426176	ESTs Weakly similar to Similar to S.cerevisiae hypothetical protein L3111 [H.sapiens]	other
32878	2.3805995259	W42789	Human terminal transferase mRNA complete cds	other
27672	2.3784145648	AA458254	ESTs	other
11623	2.3769685069	AA243617	ESTs	other
26582	2.3766957777	AA279768	ESTs	other
22142	2.3761275381	R51382	Homo sapiens mRNA for KIAA0659 protein partial cds	other
13533	2.3759359566	AA454607	ESTs Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]	other
11534	2.3747649776	AA236223	ESTs	other
5976	2.3709397882	X64229	DEK PROTEIN	other
6231	2.3680994679	X78121	Choroideremia	TM
2382	2.3677644584	M16967	Coagulation factor V	other
22887	2.3673034941	T00314	ESTs	TM
24371	2.3663729415	V87415	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	other
25286	2.3658134948	AA045281	ESTs	other
9054	2.3647542793	C02472	ESTs Weakly similar to EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1 PRECURSOR [Homo sapiens]	other
8163	2.3646144577	AA357394	ESTs	other
12233	2.3640777771	AA343513	ESTs Weakly similar to LINE/lg H-chain fusion protein [M.musculus]	SS,
22924	2.3634007127	T08195	ESTs	other
14371	2.361524453	AA599219	ESTs Moderately similar to ALR [H.sapiens]	other
12401	2.3607293844	AA400229	ESTs	other
26169	2.3599633182	AA251089	ESTs Weakly similar to ORF YOR281c [S.cerevisiae]	?
23065	2.3592943521	T23539	ESTs Highly similar to zinc finger protein [M.musculus]	other
20524	2.358218239	N53965	ESTs	other
20837	2.3577032718	N69263	ESTs Highly similar to HEXOKINASE TYPE I [Homo sapiens]	other
18201	2.3573132815	AA195398	Homo sapiens DNA sequence from PAC 43M014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1 the ADORA2B adenosine A2b receptor LIKE pseudogene the IRF6	other
7813	2.3566868562	AA248297	ESTs	TM
21195	2.3547018746	R07210	ESTs	other
13377	2.3513919997	AA449720	Homo sapiens clone 24706 mRNA sequence	other
9714	2.3497245732	L44367	ESTs	other
41537	2.3460892052	R55673	ESTs	other
17352	2.345951172	AA100925	ESTs	other
11914	2.3446813991	AA278907	ESTs	?
24890	2.3440589932	Z41634	ESTs	other
28796	2.3434458024	D91272	EST - RC_051272_s	?
36798	2.342525534	AA435870	ESTs Weakly similar to B0564.1 [C.elegans]	other
22491	2.3409294581	R70012	EST	other
4798	2.3403776443	U81538	Human calcium-binding protein cdp mRNA complete cds	other
40847	2.3397210986	N96354	ESTs	other
15657	2.3392349306	V63627	Small inducible cytokine A5 (RANTES)	TM
24482	2.3374048148	Z38137	ESTs	other
42022	2.336939603	T53138	Homo sapiens mRNA for hTCF-4	TM
38233	2.3314220199	AA489023	ESTs	other
41221	2.3310635524	R21531	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	other
8053	2.3297250374	AA309880	ESTs	other

FIGURE 8 (cont.)

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363	2.3275393529	D26528	Human mRNA for RNA helicase complete cds	?
26679	2.3241677574	AA281733	ESTs	other
13407	2.3216524472	AA450200	ESTs	TM
17955	2.3160957399	AA166703	ESTs	TM
31658	2.3160841803	N90680	EST	?
24092	2.3151511584	W42845	Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds	SS.
16759	2.3118245547	AA046294	ESTs	other
7861	2.311355404	AA252436	Homo sapiens clone 23797 and 23917 mRNA partial cds	other
41176	2.3111568743	R09379	Natural resistance-associated macrophage protein 2	TM
3860	2.3104335895	U13913	Homolog of Drosophila slowpoke (potassium channel calcium-activated)	TM
40896	2.3077403929	N68149	ESTs Weakly similar to EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1 PRECURSOR [Homo sapiens]	other
19428	2.3068982601	H22949	EST	?
36080	2.3048383557	AA417282	EST - RC_AA417282	other
27264	2.3043527378	AA418389	ESTs	other
13600	2.3031968696	AA456286	ESTs	other
13552	2.3026988375	AA454943	ESTs	other
15664	2.3025773291	W67456	ESTs Moderately similar to YY1-associated factor 2 [H.sapiens]	other
26583	2.3025403178	AA278774	ESTs	?
37434	2.3013886299	AA454149	EST	?
7833	2.2992574443	AA249300	ESTs	other
3674	2.2985613315	U05237	Human fetal Abz-50-reactive clone 1 (FAC1) mRNA complete cds	other
33694	2.2984568375	Z38770	ESTs	other
11178	2.2972286082	AA167436	ESTs	?
16977	2.2912855364	AA064616	ESTs	other
19799	2.290119924	H57330	EST	?
5948	2.2900738182	X63337	EST - X63337	?
42097	2.2881548729	T66318	Isoleucine-tRNA synthetase	?
24247	2.2881065691	W73010	Ribosomal protein L37	other
40879	2.2870463837	N67816	ESTs Moderately similar to [H] ALU SUBFAMILY SX WARNING ENTRY [H] [H.sapiens]	other
5875	2.2860441014	X59405	Membrane cofactor protein (CD46 trophoblast-lymphocyte cross-reactive antigen)	?
22325	2.2850330577	R60777	ESTs	other
9621	2.2844572929	J05032	ASPARTYL-TRNA SYNTHETASE	other
8239	2.2823045248	D79100	ESTs	other
41897	2.2818672356	T47788	ESTs	other
31105	2.28091752	N63207	EST	?
39565	2.27941194837	F04320	Replication factor C 37-kD subunit	other
7404	2.2793872556	AA094889	Homo sapiens voltage dependent anion channel protein mRNA complete cds	other
6388	2.2788870475	X85373	H.sapiens mRNA for Sm protein G	other
20283	2.2729348551	N31952	ESTs Moderately similar to HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III [Caenorhabditis elegans]	other
14528	2.2722894932	AA620307	ESTs	other
21187	2.2718368964	R07320	ESTs	other
28203	2.2682501412	AA490969	ESTs	other
38320	2.2687130032	AA490611	ESTs	other
41625	2.2680307053	R69333	ESTs	other
4674	2.265734645	U54999	Human LGN protein mRNA complete cds	other
28861	2.2637023919	D80037	EST Weakly similar to C50B8.3 [C.elegans]	other
31062	2.2633840539	N62827	ESTs	other
26756	2.2627797292	AA283832	ESTs	other
11567	2.2614480815	AA236747	Homo sapiens mitogen activated protein kinase activated protein kinase gene complete cds	other

FIGURE 8 (cont.)

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25050	2.2605083659	AA011134	ESTs Weakly similar to renin [H.sapiens]	TM
41935	2.2593192037	T29681	Human serine kinase mRNA complete cds	other
26895	2.2582367069	AA282765	H.sapiens mRNA for M-phase phosphoprotein mpp5	other
40585	2.2581993460	N34891	Homo sapiens mRNA for KIAA0585 protein partial cds	other
3343	2.2568482074	M97836	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	other
42435	2.2532463427	W46894	ESTs	?
5937	2.2469783488	X62534	High-mobility group (nonhistone chromosomal) protein 2	other
21241	2.2477801609	R08617	ESTs	TM
25756	2.2472586561	AA135866	ESTs	TM
34184	2.2458306213	AA272959	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA complete cds	other
6672	2.2450684129	AA477046	ESTs	other
7387	2.2447544716	AA093977	ESTs	other
28822	2.2424116577	D59352	ESTs	TM
18016	2.2410306445	AA173223	ESTs	other
20643	2.239288723	N69352	Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds	other
10054	2.2387950133	R10266	ESTs Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PM40-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]	other
34094	2.2384154308	AA206088	ESTs	other
41246	2.2380827238	R27296	ESTs	other
22634	2.2346537819	R82837	ESTs	other
19686	2.2319351858	H48502	ESTs	SS,
34568	2.2306030547	AA280609	ESTs Weakly similar to K02B2.3 gene product [C.elegans]	other
28448	2.2295708871	AA621752	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds	other
20909	2.2284835116	N71704	ESTs	other
651	2.2260753259	D78129	EST - D78129	SS, TM
40409	2.2244318492	H99877	Homo sapiens exportin I mRNA complete cds	other
20340	2.224062527	N38625	ESTs	other
20002	2.2233023294	H93005	EST - RC_H93005	other
37321	2.2209252793	AA451898	ESTs	other
8274	2.2208752673	AA402095	ESTs	other
20221	2.2197714812	N29345	ESTs	other
5792	2.2186801223	X54941	CDC28 protein kinase 1	other
4034	2.21808435	U21858	Human transcription initiation factor TFIIID subunit TAFII31 mRNA complete cds	other
36222	2.2149577598	AA421481	ESTs	other
16567	2.2146935655	AA031591	ESTs	other
4721	2.2134595068	U58046	Human mRNA for KIAA0139 gene complete cds	other
28656	2.2125017907	D19708	Human Gu protein mRNA partial cds	TM
20723	2.2113938194	N66093	ESTs	other
6714	2.2062571749	Y08612	H.sapiens mRNA for Nup80 protein	?
19240	2.205583996	H13285	ESTs	other
36447	2.2050784323	AA428188	ESTs	other
11688	2.202413216	AA252672	Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds	other
21650	2.2018153311	R37936	Homo sapiens KIAA0440 mRNA partial cds	other
14152	2.2015953698	AA489790	Homo sapiens Ran-GTP binding protein mRNA partial cds	other
42657	2.1975280207	V92771	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR	other
4642	2.1968027789	U52427	Human RNA polymerase II subunit hRPB7 mRNA complete cds	?
32779	2.1962611079	V02102	ESTs	TM
38341	2.1951559134	AA490967	ESTs	other
11803	2.1921143838	AA257971	ESTs	other
34835	2.190705129	AA292877	ESTs	TM
39065	2.1895804523	AA620599	ESTs	other

FIGURE 8 (cont.)

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4046	2.1877764122	U22376	MYB PROTO-ONCOGENE PROTEIN	?
11600	2.1876723705	AA242868	ESTs Weakly similar to house-keeping protein (M.musculus)	other
5051	2.1866660566	U76638	Human BRCA1-associated RING domain protein (BARD1) mRNA complete cds	other
33917	2.1864855739	AA167323	ESTs	TM
20674	2.1858972155	N63392	ESTs	TM
41031	2.1768902734	H91246	ESTs	?
25114	2.1759894688	AA020923	EST	?
24711	2.1758383153	Z39845	ESTs	other
4733	2.1721785534	U58658	Human unknown protein mRNA within the p53 intron 1 complete cds	other
4871	2.1712198791	U66033	Human glypican-5 (GPC5) mRNA complete cds	other
29733	2.1687028853	H99398	EST	?
23155	2.1678113438	T30550	ESTs	other
34638	2.164515923	AA282987	EST	?
35541	2.1621480372	AA400986	Prothymosin alpha	other
1889	2.1598384252	L20591	Annexin III (lipocortin III)	?
15106	2.1591553963	U68111	PROTEIN PHOSPHATASE INHIBITOR 2	?
40131	2.1583553082	H79779	Homo sapiens histone deacetylase 3 (HDAC3) mRNA complete cds	other
19516	2.158045763	H29207	EST	other
4136	2.1577799237	U28014	ICH-2 PROTEASE PRECURSOR	other
20276	2.1548737104	N32819	ESTs	other
13292	2.1546709291	AA447621	ESTs Highly similar to 40 KD PROTEIN (Borne disease virus)	other
20666	2.154262609	N63165	ESTs	other
6065	2.1526648242	X68560	Sp3 transcription factor	other
18238	2.1516382853	AA205389	ESTs	other
21827	2.1515899154	R37410	EST	?
3438	2.1502571642	S72024	Eukaryotic translation initiation factor 5A	?
34648	2.1498935434	AA283772	ACTIVATOR 1 39 KD SUBUNIT	other
5964	2.1488964343	X83657	Follicular lymphoma variant translocation 1	SS,
13250	2.1468085975	AA446459	ESTs	other
34370	2.1465845856	AA251829	ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MER2-CPR7 INTERGENIC REGION [Saccharomyces cerevisiae]	other
27996	2.145312871	AA470156	ESTs Weakly similar to dynein 74K chain cytosolic [R. norvegicus]	SS,
4408	2.1398865247	U41745	Human PDGF associated protein mRNA complete cds	other
4187	2.1395632136	U30888	Human tRNA-guanine transglycosylase mRNA complete cds	other
10804	2.1366859886	AA069549	ESTs	other
34552	2.1340290702	AA279985	Human mRNA for KIAA0372 gene complete cds	other
18380	2.1331897016	AA227119	ESTs	other
5223	2.1298428563	U83843	EST - U83843	other
37415	2.1270189134	AA453807	EST	other
14582	2.1260941468	AA821340	ESTs Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION [Saccharomyces cerevisiae]	other
27756	2.123647107	AA453447	ESTs	other
13787	2.1232866197	AA463745	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]	other
5173	2.1232706565	U81554	Homo sapiens signal recognition particle 72 (SRP72) mRNA complete cds	other
40029	2.1214337319	H68221	Human E2 ubiquitin conjugating enzyme UbCH5B (UBCH5B) mRNA complete cds	other
19972	2.1193721042	H83639	ESTs	other
23301	2.117519655	T52847	ESTs	other
20504	2.1134521805	N52956	ESTs	other
40145	2.1132200572	H81391	Human mRNA for histamine N-methyltransferase complete cds	other
3461	2.1131164397	S75256	EST - S75256	SS,
41893	2.1124189285	T23611	ESTs	other

FIGURE 8 (cont.)  
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39288	2.1092161318	C14805	EST - RC_C14805	other
36021	2.1064566145	AA416876	ESTs Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521 [H.sapiens]	other
8382	2.1077405638	AA424199	ESTs Weakly similar to C50B8.3 [C.elegans]	other
28288	2.1075593303	AA588447	Homo sapiens exportin 1 mRNA complete cds	other
5607	2.1071009331	X55740	5' nucleotidase (C073)	?
19747	2.106109699	H53572	ESTs	other
36155	2.1052335506	AA486777	ESTs	TM
924	2.1037724222	HG1112-HT1112	EST - HG1112-HT1112	?
8544	2.1022281514	H72630	ESTs	other
8384	2.1005713227	AA424282	Human 75-kD autoantigen (PM-Scl) mRNA complete cds	other
25165	2.1005132894	AA027837	Retinitis pigmentosa 3 (X-linked recessive)	SS, TM
24348	2.1000366836	W86469	Tropomyosin alpha chain (skeletal muscle)	?
41401	2.0994968367	R43334	Homo sapiens KIAA0410 mRNA complete cds	other
35340	2.0993782592	AA398900	EST - RC_AA398900	other
10896	2.0990741818	AA112053	ESTs Weakly similar to PRE-MRNA SPLICING HELICASE BRR2 [S.cerevisiae]	other
361	2.0974305874	D28473	Isoleucine-tRNA synthetase	other
22051	2.0971755	R49047	ESTs Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	other
3293	2.096563118	M94893	Testis specific protein Y-linked	TM
11526	2.0954548212	AA236018	ESTs Weakly similar to unknown [S.cerevisiae]	?
11690	2.0952685865	AA278323	Homo sapiens clone 24606 mRNA sequence	TM
13643	2.0952581285	AA456578	Homo sapiens clone 24477 mRNA sequence	other
19927	2.0952547855	H71829	ESTs	other
36511	2.0927695929	AA428632	ESTs	?
2130	2.0925292202	L40407	Homo sapiens thyroid receptor interactor (TRIP9) gene complete cds	?
7193	2.0924678877	AA046768	Homo sapiens clone TUA8 Cri-du-chat region mRNA	TM
5448	2.0921643167	X02751	Neuroblastoma RAS viral (v-ras) oncogene homolog	?
35956	2.0875765163	AA412533	ESTs	other
7525	2.0870133692	AA149259	ESTs	other
36592	2.0862891765	F09351	ESTs Weakly similar to weakly similar to S. cerevisiae PTM1 precursor [C.elegans]	TM
28029	2.0855736844	AA478479	ESTs	other
18425	2.0855157851	AA232103	ESTs	other
23494	2.0943308862	T70045	ESTs Weakly similar to HYPOTHETICAL 33.2 KD PROTEIN P26A3.7 IN CHROMOSOME 1 [C.elegans]	other
30882	2.0840312831	N56908	EST	?
32597	2.0839196473	T47333	Human TFIID subunit TAFII55 (TAFII55) mRNA complete cds	other
33368	2.0838178514	W60814	ESTs	other
10259	2.0829121213	R77527	ESTs	other
21882	2.0825457608	R43365	ESTs	other
20590	2.0820571859	N58146	ESTs	other
12907	2.0807802388	AA427577	ESTs	other
22958	2.0770089467	T10264	ESTs	other
42044	2.0762746251	T58753	ESTs	other
4210	2.0750374179	U31814	Human transcriptional regulator homolog RPD3 mRNA complete cds	other
39	2.074214716	AB003698	Homo sapiens mRNA for Cdc7-related kinase complete cds	other
14350	2.0739236064	AA596831	ESTs	TM
29840	2.0729224128	N21680	ESTs	other
25593	2.0715918098	AA113149	Homo sapiens IPL (IPL) mRNA complete cds	other
26071	2.0708411247	AA236880	Protein phosphatase 2A regulatory subunit B' alpha-1	other
26529	2.0699045563	AA276594	EST	?
12154	2.0692182056	AA291293	ESTs	other
16817	2.0684814007	F10077	ESTs	?

FIGURE 8 (cont.)  
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6635	2 0574931973	X99585	H. sapiens mRNA for SMT3B protein	other
6681	2.066063203	Y00971	Phosphoribosyl pyrophosphate synthetase 2	other
22077	2.0647745388	R49482	ESTs	other
11752	2.0645929355	AA256042	ESTs	other
41257	2.0634413934	R31680	ESTs	SS.
6904	2.0622381932	Z34897	Histamine receptor H1	TM
16879	2.060262971	AA056538	ESTs	other
39040	2.0595449295	AA481403	ESTs	other
4111	2.0567536207	U26312	Human heterochromatin protein HP1Hs-gamma mRNA complete cds	other
32878	2.0545812272	W37445	ESTs	TM
21743	2.0543668448	R40576	ESTs Moderately similar to IIII ALU SUBFAMILY SX WARNING ENTRY IIII [H.sapiens]	?
25968	2.0525018401	AA234935	ESTs	other
24659	2.0505511898	Z39211	Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA complete cds	other
38030	2.0505994824	AA481148	ESTs	other
61	2.0484705331	AC002115	Cytochrome c oxidase subunit Vtb	?
6305	2.0474040935	X81625	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1	?
8203	2.0473464771	AA382517	EST - AA382517	other
34357	2.0469305727	AA251430	ESTs Highly similar to RAS-RELATED PROTEIN RAB-10 [Caenorhabditis elegans]	other
36972	2.0468599712	AA442767	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein beta polypeptide	other
28156	2.0459278063	AA489057	H.sapiens mRNA for nuclear protein SA-2	?
24434	2.045695222	W92787	ESTs	other
33508	2.0449481783	W68772	Human DNA sequence from cosmid F0811 on chromosome 6. Contains Diox BING1 Tapasin RGL2 KE2 BING4 BING5 ESTs and CpG islands	other
37681	2.0448348104	AA460675	H.sapiens mRNA for TRES	other
27125	2.0448698236	AA405505	Homo sapiens mRNA for putative RNA helicase 3' end	other
3780	2.0445300752	U09851	Zinc finger protein 148 (pH2-52)	other
9112	2.0443252757	D16611	Coproporphyrinogen oxidase (coproporphyrin hemoxygenase)	TM
8357	2.044244223	AA418921	ESTs Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]	other
9133	2.0436113204	D30946	ESTs Highly similar to TRANSLOCATOR-ASSOCIATED PROTEIN GAMMA SUBUNIT [Rattus norvegicus]	TM
7519	2.0414123824	AA147425	EST - AA147425_s	other
14701	2.0413755305	D59324	ESTs	other
380	2.0411485078	D28423	EST - D28423	?
30571	2.0348528804	N49595	ESTs	other
825	2.0329522889	D87328	Holoacetylase synthetase (biotin-[propionyl-Coenzyme A-carboxylase (ATP-hydrolyzing)] ligase)	TM
27744	2.0318041265	AA452818	ESTs Weakly similar to HYPOTHETICAL PROTEIN HI0034 [Haemophilus influenzae]	other
3997	2.0311206335	U18906	Arginine vasopressin receptor 1 (AVPR1)	?
22717	2.0302732387	R81394	EST - RC_R81394	?
377	2.0289078264	D28364	EST - D28364	other
28581	2.0274006652	C21163	EST	other
11790	2.0269672127	AA256678	ESTs Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]	other
37931	2.0259058272	AA478523	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	other
24878	2.0209818539	Z39349	ESTs Weakly similar to VACUOLAR ATP SYNTHASE 54 KD SUBUNIT [Saccharomyces cerevisiae]	other
10940	2.0209035614	AA122217	ESTs Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.6 IN CHROMOSOME II [C.elegans]	other
13964	2.0207518872	AA479048	ESTs	?
15665	2.019773566	W67631	Homo sapiens clone 24538 mRNA sequence	TM
28379	2.0189373185	AA608710	ESTs	other
13349	2.0172119305	AA449269	ESTs Weakly similar to MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR [Neurospora crassa]	SS.
7322	2.0167797945	AA090692	ESTs Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]	other
29358	2.0165296752	H70641	EST - RC_H70641	?

FIGURE 8 (cont.)

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24230	2.016017502	V072276	ESTs	other
40212	2.0158778189	H88535	Human clone 121711 defective manner transposon	?
729	2.01573779	D83778	Hsma2 mRNA sequence	
17951	2.0144787235	AA165526	Human mRNA for KIAA0194 gene partial cds	other
33943	2.0135799277	AA171739	Homo sapiens bifunctional ATP sulfurylase/adenosine	other
5670	2.0118426199	X59244	5'-phosphosulfate kinase mRNA complete cds	other
36319	2.0118529739	AA425107	ESTs	other
25654	2.0097423819	AA126951	ESTs Weakly similar to DNA-directed RNA polymerase	other
16344	2.0090457727	AA018907	(D melanogaster)	?
8118	2.0090099575	AA328993	ESTs	other
29962	2.0087628098	N25228	ESTs	TM
32736	2.0078250756	R49327	Natural resistance-associated macrophage protein 2	TM
3279	2.0072427596	M94065	Dihydroorotate dehydrogenase	TM
16255	2.0065069683	AA013349	PRECURSOR	other
37972	2.0059209236	AA478215	EST - RC_AA478215	TM
41256	2.005858844	R31577	ESTs	other
34834	2.0050133743	AA292655	ESTs	other
23189	2.0039279023	T33215	ESTs	other
29851	2.0034762895	N22145	ESTs	other
32962	2	V02519	EST	?

FIGURE 8 (cont.)

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New Key Number	Accession	fold upregulated of tumor over normal colon	Unigene Descriptor	
104660	AA007160	23	ESTs	SS
130016	AA055811	14	transmembrane glycoprotein	SS, TM
104954	AA074514	10	ESTs; Moderately similar to (define not available 4753768) [H.sapiens]	Other
105082	AA143763	7	ESTs; Weakly similar to Similarity to S. Pombe BEM1/BUD5 suppressor [C.elegans]	Other
109141	AA176428	7	ESTs	Other
108893	AA135894	6	retinoic acid induced 3	TM
108927	AA143493	5	ESTs; Weakly similar to PLECKSTRIN [H.sapiens]	Other
109027	AA157818	5	Human endogenous retroviral protease mRNA; complete cds	Other
133015	AA047036	4	ESTs	Other
114546	AA056263	4	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	Other
104974	AA085918	4	H.sapiens HUNK1 mRNA	Other
108695	AA121315	4	ESTs	SS
105049	AA132554	4	ESTs; Moderately similar to myosin heavy chain 12 [H.sapiens]	Other
133834	AA147510	4	Homo sapiens serine protease mRNA; complete cds	Other
109244	AA194237	4	ESTs; Weakly similar to C17H11.6 [C.elegans]	Other
128411	AA007555	3	ESTs; Weakly similar to transformation-related protein [H.sapiens]	SS, TM
114509	AA043551	3	ESTs	Other
104888	AA053660	3	ESTs	Other
114542	AA055768	3	ESTs	SS
132718	AA056731	3	Sjogren syndrome antigen A2 (60kD; ribonucleoprotein autoantigen SS-A/Ro)	Other
104953	AA074157	3	ESTs	Other
132784	AA099589	3	GDP dissociation inhibitor 2	Other
130962	AA102051	3	transmembrane 4 superfamily member 6	SS, TM
134421	AA122386	3	collagen; type V; alpha 2	SS
105035	AA128486	3	ESTs	Other
105039	AA130349	3	ESTs	Other
105062	AA134968	3	ESTs	Other
133617	AA148318	3	Human mRNA for KIAA0069 gene; partial cds	TM

FIGURE 9

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130335	AA156499	ESTs; Highly similar to CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN [H.sapiens]	Other
105132	AA159501	HBV associated factor	Other
109042	AA159525	ESTs	Other
109043	AA159605	ESTs	Other
132669	AA188378	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN L22 [H.sapiens]	Other
135398	AA194075	nuclear receptor coactivator 4	Other
109344	AA213696	ESTs	SS
133221	AA235289	ESTs; Highly similar to rap2 gene product [H.sapiens]	Other
114496	AA035611	ESTs; Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	Other
128635	AA043959	tropomyosin 4	Other
129912	AA047344	ESTs; Weakly similar to similar to WW/rsp5/WWP domain containing proteins [C.elegans]	Other
104927	AA058855	ESTs	SS
132821	AA070724	CD44 antigen (homing function and Indian blood group system)	Other
108409	AA075578	zm88h3.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:54545 3', mRNA sequence"	Other
133621	AA076138	H2A histone family; member Y	Other
108565	AA085342	ATPase; Ca++ transporting; cardiac muscle; slow twitch 2	TM
104977	AA088228	ESTs	Other
103777	AA093131	Homo sapiens PAC clone DJ0167F23 from 7p15	Other
108649	AA112540	ESTs	Other
114692	AA121995	ESTs; Weakly similar to Similar to potassium channel protein. [C.elegans]	Other
105063	AA134985	ESTs	Other
133273	AA147725	dendritic cell protein	Other
128515	AA149044	ESTs; Highly similar to the KIAA0195 gene is expressed ubiquitously. [H.sapiens]	SS
105182	AA191014	ESTs; Weakly similar to Ydr372cp [S.cerevisiae]	Other
109277	AA196332	ESTs	Other
132608	AA199588	ARP3 (actin-related protein 3; yeast) homolog	Other
109380	AA219015	ESTs	Other
130800	AA223386	ESTs; Weakly similar to katanin p80 subunit [H.sapiens]	Other
129945	AA232104	ESTs; Highly similar to (define not available 4929579) [H.sapiens]	Other
105305	AA233609	spindle pole body protein	Other

FIGURE 9

(Cont.)

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128924	AA234962	2 ESTs	TM
114895	AA236177	Homo sapiens mRNA for KIAA0887 protein; 2' partial cds	Other

## FIGURE 9 (Cont.)

FIGURE 10  
1 of 8

	A	B	C	D	E
1	1999 New Key/Num	2000 over/normal	2001	2002	2003
2	2451	52.6	M21305	Human alpha satellite and satellite 3 junction DNA sequence	?
3	27090	7.4	AA11502	ESTs; Weakly similar to serine protease [H.sapiens]	?
4	232	7	D13666	Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)	SS
5	25461	6.8	AA102520	ESTs; Weakly similar to heat shock protein hsp4 homolog [H.sapiens]	TM
6	27665	6.2	AA453783	ESTs	other
7	39492	6.2	F13673	ESTs	other
8	28050	5.6	AA489057	H.sapiens mRNA for nuclear protein SA-2	?
9	31485	5.6	NT1781	ESTs	other
10	25608	5.4	AA132514	density-regulated protein	other
11	7000	5	Z14816	collagen, type I, alpha 2	SS
12	25931	4.7	AA236200	ESTs	other
13	12118	4.5	AA291528	ESTs	other
14	32913	4.4	V46810	HMT1 (hMRNP methyltransferase; S. cerevisiae)-like 2	other
15	26684	4.3	AA393804	H beta 58 homolog	other
16	22514	4.2	RT9392	ESTs	other
17	25466	4.2	AA112012	lactate dehydrogenase A	TM
18	32276	4.1	R92994	mainly metalloproteinase 12 (macrophage elastase)	SS
19	32465	4.1	T32108	ESTs	other
20	22430	4	RT1082	TFAR19 novel apoptosis-related gene	other
21	30052	4	N32586	ESTs; Weakly similar to Yrd33p [S.cerevisiae]	?
22	28354	3.9	C14037	ESTs; Weakly similar to Yef7c-ap [S.cerevisiae]	?
23	28604	3.9	H96555	Homo sapiens gene for NBS1; complete cds	TM
24	27592	3.8	AA449417	Homo sapiens mRNA for putative glucosyltransferase; partial cds	TM
25	28691	3.8	D51276	STATHMIN	other
26	19100	3.7	H10933	ESTs	other
27	5891	3.5	X60486	H4 histone family; member G	?
28	12286	3.5	AA398243	ESTs; Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]	other
29	23628	3.5	T68700	ESTs	other
30	25951	3.5	AA236672	ESTs; Weakly similar to DFS7 [H.sapiens]	other
31	4177	3.4	D35833	Human mRNA for calgizzarin, complete cds	?
32	11193	3.4	AA186897	ESTs	TM
33	27193	3.4	AA421562	Homo sapiens secreted cement gland protein XAG-2 homolog (XAG-2IR)	SS
34	32899	3.4	W45726	ESTs; Highly similar to HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN	other
35	9576	3.3	J03464	collagen, type I, alpha 2	SS
36	10506	3.3	AA027086	ESTs; Highly similar to HYPOTHETICAL 1.4 KD PROTEIN IN UBPS-SPT	other
37	22064	3.3	R51309	ESTs	other
38	39217	3.3	C21242	calponin 2	other
39	2613	3.2	M29540	CARCINOEMBRYONIC ANTIGEN PRECURSOR	TM
40	27583	3.2	AA448068	ESTs	TM
41	40031	3.2	H83442	calicheal-O-methyltransferase	other
42	10131	3.1	R36183	eukaryotic translation initiation factor 3; subunit 6 (48kD)	other
43	25154	3.1	AA043353	ESTs; Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD	other
44	25621	3.1	AA164643	ESTs; Weakly similar to K-167 intracellular antigen [H.sapiens]	other

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FIGURE 10 (CONT)

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	A	B	C	D	E
45	26004	3.1	AA243297	ESTs; Weakly similar to PEANUT PROTEIN [Drosophila melanogaster]	other
46	27055	3.1	AA065542	ESTs	other
47	10844	3	AA100719	non-specific cross reacting antigen	other
48	11358	3	AA232104	ESTs	other
49	17389	3	AA121315	ESTs	other
50	17415	3	AA122386	Collagen, type V, alpha 2	7
51	23772	3	192735	ESTs	TM
52	25331	3	AA070947	Inopomyosin 4	other
53	25358	3	AA076138	histone macroH2A1.2	other
54	27039	3	AA406145	ESTs	SS, TM
55	27261	3	AA425544	Homo sapiens clone 23649 mRNA, complete cds	other
56	28795	3	D80946	SFRS protein kinase 1	other
57	32192	3	R61275	collagen, type XI, alpha 1	other
58	3003	2.9	M77349	transforming growth factor, beta-induced; 68KD	SS
59	5519	2.9	X06700	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV; autosomal do	other
60	5562	2.9	X12876	keratin 18	other
61	11618	2.9	AA251902	Homo sapiens lysophospholipase (LPL) mRNA, complete cds	other
62	17868	2.9	AA147725	Homo sapiens GAT7 protein mRNA, complete cds	other
63	18024	2.9	AA188376	ESTs; Highly similar to 6S RIBOSOMAL PROTEIN L22 [Rattus norvegicu	other
64	20941	2.9	N09633	ESTs	other
65	13612	2.8	AA458899	ESTs; Highly similar to (define not available 412715) [H.sapiens]	TM
66	17799	2.8	AA157818	Human endogenous retroviral protease mRNA, complete cds	other
67	25344	2.8	AA075182	Sjogren syndrome antigen A2 (6kD; ribonucleoprotein autoantigen SS-A/R	7
68	25583	2.8	AA131162	ESTs	other
69	37170	2.8	R51297	eukaryotic translation initiation factor 3; subunit 6 (48KD)	other
70	33656	2.8	Z36556	coatomer protein complex; subunit alpha	SS
71	3296	2.7	M18728	non-specific cross reacting antigen	other
72	3251	2.7	M93036	membrane component chromosomal 4; surface marker (35KD glycoprotein	other
73	8158	2.7	AA372630	Homo sapiens GWT12 protein (GWT12) mRNA, complete cds	other
74	9207	2.7	D79552	ESTs; Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 GAMM	other
75	15051	2.7	U84661	Human poly(A)-binding protein processed pseudogene3	?
76	15814	2.7	V53627	ESTs; Moderately similar to IIII ALU SUBFAMILY SP WARNING ENTRY II	TM
77	25323	2.7	AA070465	Homo sapiens clone 23967 unknown mRNA; partial cds	other
78	25329	2.7	AA070827	ESTs; Weakly similar to KIAA18 [H.sapiens]	TM
79	25549	2.7	AA127058	ESTs; Weakly similar to predicted using Genefinder [C.elegans]	TM
80	25584	2.7	AA131165	Heterogeneous nuclear ribonucleoprotein A2/B1	other
81	27483	2.7	AA441971	Homo sapiens mRNA for KIAA494 protein, complete cds	TM
82	32012	2.7	R31160	ESTs	?
83	38087	2.7	AA468991	Homo sapiens chaperonin containing 1-complex polypeptide 1; beta subunit	other
84	38437	2.7	AA589714	Lon protease-like protein	other
85	39421	2.7	F03974	H.sapiens mRNA for Sop2p-like protein	other
86	3758	2.6	U09587	glycyl-tRNA synthetase	other
87	8952	2.6	C00038	ESTs	TM
88	12978	2.6	AA431191	ESTs	other

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FIGURE 10 (CONT)  
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A	B	C	D	E
89	17627	AA135894	Homo sapiens putative G protein-coupled receptor (RAUG1). Retinoic acid i	TM
90	20752	N68921	ESTs; Weakly similar to neogenin [H.sapiens]	other
91	22954	T17185	ESTs	TM
92	25608	AA161161	ESTs	other
93	27169	AA418879	proteasome (prosome; macropain) 26S subunit; non-ATPase; 11	other
94	28086	AA490962	ESTs; Moderately similar to ubiquitous TPR motif; Y isoform [H.sapiens]	other
95	28705	D54289	ESTs	other
96	33593	Z39041	ESTs; Weakly similar to DNA-DIRECTED RNA POLYMERASE III LARGE	TM
97	37363	AA455521	E2F transcription factor 5; p13-binding	other
98	39170	C15324	ESTs	SS TM
99	39251	D20002	HUMGS972 Human promyelocyte Homo sapiens cDNA clone pm2344.3;	other
100	2767	A375893	H2A histone family, member Z	other
101	5468	X04347	heterogeneous nuclear ribonucleoprotein A1	other
102	9243	D62348	Homo sapiens mRNA for 5-aminimidazole-4-carboxamide-1-beta-D-ribo	other
103	14791	T35725	ESTs; Highly similar to HYPOTHETICAL 44.2 KD PROTEIN IN SCO2.MR	other
104	14804	148195	eukaryotic translation initiation factor 3; subunit 3 (gamma; 4kD)	other
105	16974	AA070724	CD44 antigen (homolog function and Indian blood group system)	other
106	20031	N21085	Homo sapiens androgen receptor associated protein 24 (ARAZ4) mRNA; c	?
107	25484	AA112679	ESTs; Weakly similar to alternatively spliced product using exon 13A [H.sa	TM
108	28830	AA347359	lysosome (renal amyloidosis)	SS
109	28058	AA480212	histone macroH2A1.2	other
110	30071	N33011	replication protein A3 (14kD)	other
111	32740	V31600	von Hippel-Lindau syndrome	other
112	35870	AA416765	heterogeneous nuclear ribonucleoprotein A1	other
113	41908	T59161	Thymosin; beta 1	TM
114	6011	X66401	proteasome (prosome; macropain) subunit; beta type; 9 (large multifunctio	?
115	9201	D63079	ESTs; Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAI	other
116	9218	D79891	ESTs	TM
117	10985	R32993	ESTs; Highly similar to LEUCYL-TRNA SYNTHETASE; CYTOPLASMIC [	other
118	10253	R82411	DEK gene	other
119	11107	AA159501	ESTs; Moderately similar to RBCK2 [R.norvegicus]	other
120	11846	AA262969	ESTs; Weakly similar to similar to Yeast hypothetical protein L8187.12 like	other
121	12767	AA424346	ESTs; Weakly similar to unoporphyrinogen III synthase; UROIII [H.sapien	SS
122	13772	AA464708	ESTs; Weakly similar to alternatively spliced product using exon 13A [H.sa	other
123	16728	AA053102	cadherin 17; LI cadherin (liver-intestine)	SS TM
124	17774	AA156243	ESTs; Highly similar to (define not available 412715) [H.sapiens]	other
125	21385	R24059	ESTs	other
126	25433	AA095589	GDP dissociation inhibitor 2	TM
127	25603	AA132032	Homo sapiens CAGH1a (CAGH1) mRNA; partial cds	other
128	25781	AA159980	ELK motif kinase	other
129	26153	AA252627	ESTs	?
130	26552	AA365527	ESTs; Weakly similar to TLS-associated protein TASR [H.sapiens]	other
131	21122	AA416877	ESTs	other
132	28365	C14090	actin; gamma 1	other

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FIGURE 10 (CONT)  
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	A	B	C	D	E
133	26528	2.4	D5560	Homo sapiens DNA from chromosome 19-co-samid R3979 containing USF2	other
134	26607	2.4	D51241	Homo sapiens mRNA for putative vacuolar proton ATPase membrane sect	SS, TM
135	29850	2.4	N24960	vacuolar H(+)-ATPase subunit	other
136	32892	2.4	W45457	ESTs: Moderately similar to neuronal thread protein AD7c-NTP [H. sapiens]	other
137	33811	2.4	AA173143	heterogeneous nuclear ribonucleoprotein G	other
138	40121	2.4	H93492	ESTs: Highly similar to villin [H. sapiens]	other
139	40141	2.4	H94877	ESTs: Moderately similar to putative G-binding protein [H. sapiens]	other
140	40167	2.4	H96237	collagen, type XI, alpha 1	other
141	446	2.3	D38073	mitochondrion maintenance deficient (S. cerevisiae) 3	other
142	3530	2.3	S81914	DIFFERENTIATION-DEPENDENT GENE 2	other
143	7835	2.3	AA252436	Homo sapiens lysophospholipase (LPL1) mRNA, complete cds	other
144	10938	2.3	AA121879	proteasome (prosome; macropain) subunit, beta type, 9 (large multifunction	other
145	10965	2.3	AA134138	ESTs: Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]	other
146	11015	2.3	AA143783	ESTs: Weakly similar to similarity to S. Pombe BEM1/UD5 suppressor [C	other
147	11895	2.3	AA279420	ESTs: Highly similar to (define not available 433735) [H. sapiens]	TM
148	13386	2.3	AA451678	ESTs	other
149	15464	2.3	W28391	proliferation-associated 2G4, 38kD	other
150	17619	2.3	AA135406	ESTs	other
151	18235	2.3	AA213696	ESTs	other
152	20450	2.3	N33927	ESTs: Weakly similar to phenylalanine binding protein [H. sapiens]	?
153	25308	2.3	AA065227	ESTs: Weakly similar to coded for by C. elegans cDNA yk1c1.3 [C. elegans	other
154	28590	2.3	AA282151	ESTs: Weakly similar to predicted using GeneFinder [C. elegans]	other
155	27624	2.3	AA452112	Homo sapiens mRNA for putative thionin-like protein	other
156	27792	2.3	AA460359	ESTs: Weakly similar to DNA-DIRECTED RNA POLYMERASE II 14 KD P	?
157	28231	2.3	AA600153	DEK gene	other
158	28722	2.3	D59711	ESTs	other
159	30363	2.3	N47856	eukaryotic translation initiation factor 3, subunit 3 (gamma, 4kD)	other
160	32928	2.3	W47620	ESTs: Weakly similar to reverse transcriptase related protein [H. sapiens]	other
161	39585	2.3	H11320	Homo sapiens HRIHFB2115 mRNA, partial cds	TM
162	40175	2.3	H96655	peptidylprolyl isomerase B (cyclophilin B)	other
163	40366	2.3	N76691	ESTs: Highly similar to (define not available 467914) [H. sapiens]	other
164	40733	2.3	N67422	ESTs: Weakly similar to 25 kDa trypsin inhibitor [H. sapiens]	other
165	4918	2.2	U68105	poly(A)-binding protein-like 1	?
166	5165	2.2	U81607	GRAVIN	other
167	12242	2.2	AA372018	ESTs	other
168	13154	2.2	AA447168	Homo sapiens inner mitochondrial membrane translocase Tim23 (TIM23)	?
169	14276	2.2	AA594450	ESTs	other
170	15721	2.2	W95348	ESTs	TM
171	20598	2.2	N62945	Homo sapiens tRim TRA1b mRNA, complete cds	TM
172	24021	2.2	W42657	ESTs	other
173	24250	2.2	W84712	calumenin	other
174	25245	2.2	AA055768	ESTs	SS
175	25430	2.2	AA099429	SPlicing FACTOR U2AF 35 KD SUBUNIT	TM
176	25562	2.2	AA128904	heterogeneous nuclear ribonucleoprotein U (scalloid attachment factor A)	other

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FIGURE 10 (CONT)  
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	A	B	C	D	E
177	28745	2.2	D60485	caldesmon 1	other
178	31897	2.2	R20669	tumor rejection antigen (gp98) 1	other
179	32491	2.2	T47333	Human TFIIID subunit TAF <sub>II</sub> 155 (TAF <sub>II</sub> 155) mRNA; complete cds	other
180	32636	2.2	T93007	high-mobility group (nonhistone chromosomal) protein 1	other
181	37703	2.2	AA476237	ESTs; Weakly similar to uroporphyrinogen III synthase; UROIIIIS [H.sapien]	TM
182	215	2.1	D13627	Human mRNA for KIAA2 gene; complete cds	TM
183	2449	2.1	M21259	small nuclear ribonucleoprotein polypeptide E	?
184	3205	2.1	M88458	ER LUMEN PROTEIN RETAINING RECEPTOR 2	TM
185	4197	2.1	U31556	E2F transcription factor 5; p13-binding	other
186	4811	2.1	U62982	eukaryotic translation initiation factor 3; subunit 8 (48kD)	other
187	5417	2.1	X01060	transferrin receptor (p8; CD71)	TM
188	6334	2.1	X63228	cadherin 17; LI cadherin (liver-intestine)	SS TM
189	6805	2.1	X99133	NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR	?
190	10471	2.1	AA024482	ESTs; Highly similar to KERATIN; TYPE I CYTOSKELETAL 14 [Homo sa]	other
191	11027	2.1	AA148318	Human mRNA for KIAA69 gene; partial cds	TM
192	11116	2.1	AA161282	INTERFERON-ALPHA INDUCED 1.5 KO PROTEIN	other
193	11540	2.1	AA236972	ESTs; Moderately similar to H1ALU SUBFAMILY J WARNING ENTRY IIII	other
194	11937	2.1	AA280865	ESTs; Weakly similar to Similarly to Yeast hypothetical protein YOR3160	other
195	17312	2.1	AA111869	pigment epithelium-derived factor	other
196	19286	2.1	H16847	ESTs	other
197	20122	2.1	N26259	ESTs; Weakly similar to uroporphyrinogen III synthase; UROIIIIS [H.sapien]	other
198	20346	2.1	N91492	Homo sapiens clone 628 unknown mRNA; complete sequence	other
199	20997	2.1	N98464	ESTs	other
200	27106	2.1	AA124452	ESTs	other
201	28036	2.1	AA488433	ESTs; Weakly similar to deduced amino acid sequence is highly homologous	other
202	28167	2.1	AA321256	ESTs; Highly similar to nuclear pore complex protein NUP17 [R.norvegicus]	other
203	28336	2.1	AA021604	ESTs	other
204	28719	2.1	D59570	ESTs	other
205	28886	2.1	F04674	Homo sapiens mRNA for KIAA746 protein; partial cds	other
206	32124	2.1	R48608	eukaryotic translation initiation factor 3; subunit 7 (beta; 66kD)	other
207	33433	2.1	W90444	ESTs; Highly similar to (define not available 4454524) [H.sapiens]	other
208	33564	2.1	W96151	ESTs; Moderately similar to ganglioside-induced differentiation associated	?
209	35778	2.1	AA412270	ESTs	other
210	38588	2.1	AA508751	cathepsin B	other
211	39301	2.1	D57317	Human transcriptional coactivator PCA mRNA; complete cds	SS
212	39945	2.1	H73484	ESTs; Weakly similar to Yeast hypothetical protein L6167.12 like	SS TM
213	39977	2.1	H78323	Homo sapiens E2F-related transcription factor (DP-1) mRNA; complete cds	other
214	40376	2.1	N27198	ESTs	other
215	41795	2.1	T28759	ESTs; Highly similar to TYROSINE-PROTEIN KINASE RECEPTOR EPH-	TM
216	1714	2	L09604	proteolipid protein 2 (colon epithelium-enriched)	TM
217	2001	2	L33930	Homo sapiens CD24 signal transducer mRNA; complete cds and 3' region	TM
218	3278	2	M94556	single-stranded DNA-binding protein	other
219	4145	2	U28749	High-mobility group (nonhistone chromosomal) protein isoform 1-C	TM
220	8149	2	AA364267	ESTs; Highly similar to HYPOTHETICAL 68.7 KO PROTEIN ZK757.1 IN C	other

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FIGURE 10 (CONT)  
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	A	B	C	D	E
221	9844	2	N33807	ESTs: Highly similar to MEDD-4 PROTEIN [Homo sapiens]	other
222	14032	2	AA466092	ESTs: Weakly similar to CH-TOG PROTEIN [H. sapiens]	TM
223	18395	2	AA025673	ESTs: Moderately similar to (define not available 416376) [H. sapiens]	TM
224	17327	2	AA112540	ESTs	TM
225	23083	2	T30881	ubiquitin-conjugating enzyme E2E 1 (homologous to yeast UBC4/5)	other
226	25625	2	AA133969	ESTs: Weakly similar to neuronal thread protein AD7C-ATP [H. sapiens]	other
227	28073	2	AA490494	ESTs	other
228	28700	2	D53139	ribosomal protein S28	other
229	28095	2	H27188	collagen-binding protein 2 (collagen 2)	other
230	32191	2	R67083	calnexin	SS, TM
231	32897	2	W45564	5' nucleotidase (CD73)	other
232	10782	1.6	AA074880	ESTs: Weakly similar to HYPOTHETICAL 65_KD PROTEIN IN CPA2-ATP	other
233	27795	1.6	AA460454	ESTs: Weakly similar to KIAA512 protein [H. sapiens]	other
234	28706	1.6	D54298	Human mRNA for KIAA255 gene; complete cds	TM
235	36414	1.6	AA430186	ESTs	other
236	9979	1.5	N91067	ESTs: Weakly similar to F5SA12.9 [C. elegans]	other
237	9937	1.5	N95507	ESTs: Weakly similar to KIAA319 [H. sapiens]	TM
238	10656	1.5	AA047290	ESTs	other
239	14977	1.5	U37546	apoptosis inhibitor 1	TM
240	27085	1.5	AA110294	Human mRNA for KIAA336 gene; complete cds	other
241	29278	1.5	H72948	biglycan	SS
242	31917	1.5	N98238	ESTs	other
243	38272	1.5	AA495533	ESTs	other
244	41398	1.5	R55342	CD68 antigen	other
245	41966	1.5	T67710	ESTs	?
246	8439	1.4	AA436304	Homo sapiens androgen receptor associated protein 24 (ARA24) mRNA; c	other
247	10311	1.4	AA001936	ESTs	other
248	10859	1.4	AA112149	ESTs	other
249	11279	1.4	AA213410	ESTs	SS
250	13548	1.4	AA456033	ESTs: Highly similar to HYPOTHETICAL 1.4_KD PROTEIN IN UBPS-SPT	other
251	14340	1.4	AA598653	Homo sapiens TCFL5 mRNA for transcription factor-like 5; complete cds	other
252	32160	1.4	R63727	ESTs	other
253	35187	1.4	AA398722	ESTs	other
254	37254	1.4	AA453483	ESTs	TM
255	1344	1.3	HG4757-HT5207	"Oncogene Mit-A4, Fusion Activated"	other
256	5397	1.3	V01516	KERATIN TYPE II CYTOSKELETAL 6D	SS, TM
257	16272	1.3	AA018922	core promoter element binding protein	other
258	23427	1.3	T70358	ESTs: Highly similar to POL POLYPROTEIN [Simian sarcoma virus]	other
259	25718	1.3	AA150741	gene with multiple splice variants near HD locus on 4p16.3	other
260	33499	1.3	W93403	ESTs	other
261	36374	1.3	AA434454	ESTs: Weakly similar to orf; hypothetical protein [E. coli]	SS
262	41548	1.3	R82846	ESTs	other
263	2386	1.2	M17863	Insulin-like growth factor 2 (somatomedin A)	TM
264	6383	1.2	X65371	lethal giant larvae [Drosophila] homolog 1	other

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FIGURE 10 (CONT)  
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	A	B	C	D	E
265	24427	1.2	Z39208	ESTs	other
266	27089	1.2	AA411473	adducin 1 (alpha)	other
267	33177	1.2	W73195	ESTs	other
268	34852	1.2	AA347691	ESTs	?
269	35325	1.2	AA400273	ESTs	other
270	36609	1.2	AA435668	ESTs, Weakly similar to pxdalve p15 [H.sapiens]	other
271	38477	1.2	AA598939	ESTs	other
272	40975	1.2	R02547	ESTs	other
273	41874	1.2	T51150	ESTs	other
274	8235	1.1	AA401047	Homo sapiens mRNA for neuropilin, complete cds	other
275	9772	1.1	M81349	SERUM AMYLOID A-4 PROTEIN PRECURSOR	SS
276	14756	1.1	S83198	BPLP	other
277	15831	1.1	X90579	H.sapiens DNA for cyp related pseudogene	?
278	20656	1.1	N62289	ESTs	other
279	24891	1.1	AA004502	carcinoside (3'-phosphoadenylylsulfate:galactosylceramide 3') sulfoltransfer	TM
280	29045	1.1	H13549	ESTs	other
281	31584	1.1	N74690	ESTs	TM
282	31640	1.1	N78784	Homo sapiens Bin1L mRNA, complete cds	other
283	35293	1.1	AA400013	EST	other
284	37583	1.1	AA461499	ESTs	other
285	37852	1.1	AA479896	ESTs	other
286	38397	1.1	AA521342	ESTs	other
287	38652	1.1	AA609018	ESTs	other
288	40397	1.1	N29963	ESTs; Moderately similar to III ALU CLASS C WARNING ENTRY III [H.sapiens]	other
289	40488	1.1	N40559	ESTs; Highly similar to LEUKOTOXIN SECRETION ATP-BINDING PROT	other
290	41231	1.1	R41772	EST	other
291	41333	1.1	R48590	ESTs	other
292	3255	1	M93143	Homo sapiens plasminogen-like protein (PLG) mRNA, complete cds*	other
293	5742	1	X53065	Accession not listed in Genbank	?
294	6007	1	X66363	SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1	other
295	15233	1	W04960	ESTs	other
296	15282	1	W17304	Homo sapiens mRNA for KIAA97 protein, complete cds	other
297	15363	1	W26947	ESTs; Highly similar to MITOCHONDRIAL RNA SPLICING PROTEIN MS	other
298	15606	1	W58725	mitogen-activated protein kinase-activated protein kinase 2	TM
299	18435	1	AA233698	ESTs	other
300	21796	1	R41999	ESTs	TM
301	25306	1	AA065081	*m13a2.s1 Stralagene pancreas (#93728) Homo sapiens cDNA clone IMA	other
302	29111	1	H40486	ESTs; Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	other
303	34743	1	AA302772	ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	other
304	34801	1	AA342526	ESTs; Moderately similar to unknown [H.sapiens]	other
305	35355	1	AA405521	ESTs	other
306	36940	1	AA468449	ESTs	other
307	38221	1	C21330	ESTs	other
308	1322	0.9	HG4535-H14940	Demain	other

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FIGURE 10 (CONT)  
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	A	B	C	D	E
309	9882	0.9	N94146	ESTs	other
310	10084	0.9	R32932	ESTs	other
311	11701	0.9	AA255546	ESTs	other
312	12088	0.9	AA287566	Human mRNA for KIAA187 gene; complete cds	other
313	15267	0.9	W19098	ESTs	other
314	15901	0.9	Z29905	immunoglobulin superfamily, member 3	SS
315	21906	0.9	R45512	ESTs	other
316	22002	0.9	R49459	ESTs	other
317	23136	0.9	T40827	ESTs	other
318	28673	0.9	D45719	ESTs	other
319	29159	0.9	H60324	ESTs	other
320	32810	0.9	T89122	Human clone 23732 mRNA; partial cds	SS, TM
321	32674	0.9	W02129	EST	other
322	35426	0.9	AA401409	ESTs	other
323	38504	0.9	AA599209	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H sapiens]	other
324	244	0.8	D14446	fibronogen-like 1	TM
325	14204	0.8	AA496980	ESTs	other
326	25250	0.8	AA056210	ESTs	other
327	9371	0.7	N87590	ESTs	other
328	20461	0.7	N54429	ESTs	other
329	41029	0.7	R08615	homogenisale 1,2-dioxygenase (homogenisale oxidase)	other
330	41985	0.6	T71012	fibronogen; B beta polypeptide	SS, TM

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
134804	12.3	L37036	small inducible cytokine subfamily B (Cys-X-Cys); member 5 (epithelial-derived neutrophil-activating peptide 78)	TM
130617	11.4	M90516	glutamine-fructose-6-phosphate transaminase 1	TM
104209	10.6	AB000221	small inducible cytokine subfamily A (Cys-Cys); member 18; pulmonary and activation-regulated	SS
109991	10	H09813	ESTs	TM
124315	8.3	H94892	v-rat simian leukemia viral oncogene homolog A (ras related)	Other
132977	8.2	U28686	RNA binding motif protein 3	Other
130407	7.4	N29888	ESTs	Other
116176	6.6	AA463725	ESTs; Weakly similar to KIAA0226 [H.sapiens]	Other
119271	6.5	T16387	ESTs	Other
134711	6.5	X04011	cytochrome b-245; beta polypeptide (chronic granulomatous disease)	TM
134326	6.1	U16306	"Human chondroitin sulfate proteoglycan versican V splice-variant precursor peptide mRNA, complete cds"	Other
125852	5.9	H09290	ESTs; Weakly similar to unknown [H.sapiens]	SS, TM
112169	5.9	R48589	ESTs	TM
132528	5.9	AA283008	chromosome-associated polypeptide C	Other
134367	5.7	X54199	phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide synthetase; phosphoribosylaminimidazole synthetase	Other
111929	5.2	R40057	prominin (mouse)-like 1	SS, TM
102165	5	U18321	Death associated protein 3	Other
130441	5	U35835	protein kinase; DNA-activated; catalytic polypeptide	Other
133282	5	U52960	SRB7 (suppressor of RNA polymerase B; yeast) homolog	Other
100783	4.9	HG3748-HT4 018	"Basic Transcription Factor, 44 Kda Subunit"	Other
122223	4.9	AA436158	ESTs	Other
104660	4.8	AA007160	ESTs	SS
113702	4.8	T97307	ESTs; Moderately similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	Other
101185	4.7	L19872	aryl hydrocarbon receptor	Other
105308	4.7	AA233744	ESTs	Other
107168	4.7	AA621540	ESTs	Other
101201	4.6	L22524	matrix metalloproteinase 7 (matrilysin; uterine)	SS
101809	4.5	M86849	"Homo sapiens connexin 26 (GJB2) mRNA, complete cds"	TM
101478	4.5	M23379	RAS p21 protein activator (GTPase activating protein) 1	Other
104695	4.5	AA012953	ESTs	Other
100365	4.4	D78611	mesoderm specific transcript (mouse) homolog	TM
126819	4.3	AA305538	"EST176522 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end, mRNA sequence."	Other
101880	4.3	M97925	defensin; alpha 5; Paneth cell-specific	SS
126838	4.2	AA858097	pigment epithelium-derived factor	Other
101684	4.2	M63256	cerebellar degeneration-related protein (62kD)	Other
117634	4.2	N36421	ESTs; Moderately similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	Other
132109	4.1	AA595801	ESTs	Other
115054	4.1	AA252863	ESTs	Other
106553	4	AA454967	ESTs	Other
119717	3.9	W69134	ESTs	Other

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## FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated In Tumors	Exemplar Accession	Complete Title	ORF Structural Info
131945	3.9	M87339	replication factor C (activator 1) 4 (37kD)	Other
128790	3.9	AA291725	secreted frizzled-related protein 4	SS
120562	3.8	AA280036	ESTs; Weakly similar to W01A6.c [C.elegans]	SS
109517	3.7	D60799	ESTs	Other
102618	3.7	U65932	extracellular matrix protein 1	SS
106286	3.7	AA434441	frizzled (Drosophila) homolog 7	Other
133640	3.6	D83004	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)	Other
100335	3.6	D63391	platelet-activating factor acetylhydrolase; isoform 1b; gamma subunit (29kD)	Other
104720	3.6	AA018441	ESTs	Other
107348	3.6	U43701	ribosomal protein L23a	Other
134989	3.6	AA236324	ESTs; Weakly similar to IIII ALU CLASS A WARNING ENTRY IIII [H.sapiens]	SS
111345	3.6	N89820	ESTs	Other
107053	3.6	AA600147	ESTs; Weakly similar to Similar to NADH-cytochrome B5 reductase [C.elegans]	Other
107240	3.5	D59368	ESTs	Other
107129	3.5	AA620553	flap structure-specific endonuclease 1	Other
134846	3.5	AA431505	Homo sapiens mRNA for putative Sqv-7-like protein; partial	TM
101897	3.5	S58544	sperm associated antigen 1	Other
107151	3.5	AA621169	ESTs	Other
106012	3.4	AA411621	ESTs	Other
101950	3.4	S79219	propionyl Coenzyme A carboxylase; alpha polypeptide	Other
116844	3.4	H64938	ESTs	Other
128025	3.4	AA937173	ESTs	TM
106785	3.4	AA478587	leukemia associated gene 1; candidate tumor suppressor frequently deleted in B-cell chronic lymphocytic leukemia (B-CLL)	Other
104518	3.4	R09815	proteasome (prosome; macropain) 26S subunit; ATPase; 5	Other
117667	3.4	N39214	ser-Thr protein kinase related to the myotonic dystrophy protein kinase	Other
104954	3.3	AA074514	ESTs; Moderately similar to (define not available 4753768) [H.sapiens]	Other
105372	3.3	AA236481	ESTs	Other
104896	3.3	AA054228	ESTs	Other
113485	3.3	T87863	ESTs	Other
127003	3.3	AA550806	ESTs; Weakly similar to (define not available 3882151) [H.sapiens]	TM
100305	3.3	D50487	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase)	SS
134722	3.2	W47183	ESTs; Weakly similar to IIII ALU SUBFAMILY SB2 WARNING ENTRY IIII [H.sapiens]	Other
126801	3.2	AA512902	ESTs	SS, TM
133503	3.2	M33195	Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide	SS, TM
132183	3.2	L19183	Human MAC30 mRNA; 3' end	TM
105298	3.2	AA233459	ESTs	TM
111046	3.2	N55514	ESTs; Moderately similar to IIII ALU SUBFAMILY SP WARNING ENTRY IIII [H.sapiens]	TM
135309	3.2	D25984	ESTs	SS
102808	3.2	U90426	nuclear RNA helicase; DEAD variant of DEAD box family	Other
100552	3.1	HG2167-HT2 237	"Protein Kinase Ht13, Camp-Dependent"	Other
127652	3.1	AA804487	ESTs	Other

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## FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated In Tumors	Exemplar Accession	Complete Title	ORF Structural Info
116127	3.1	AA459703	ESTs; Moderately similar to coded for by C. elegans cDNA CEESD64F [C.elegans]	TM
131904	3.1	AA143019	ESTs; Highly similar to surface 4 Integral membrane protein [H.sapiens]	TM
126547	3.1	U47732	transmembrane 4 superfamily member 3	Other
102823	3.1	U90914	carboxypeptidase D	SS
132298	3.1	N41849	Homo sapiens cytokine receptor related protein 4 (CYTOR4) mRNA; complete cds	Other
127445	3.1	AA906286	ESTs	Other
134395	3.1	L09717	lysosomal-associated membrane protein 2	SS, TM
105743	3.1	AA293300	ESTs; Weakly similar to semaphorin C [M.musculus]	Other
125827	3.1	AJ471525	YY1 transcription factor	Other
101229	3.1	L27943	cytidine deaminase	Other
102306	3	U33317	defensin; alpha 6; Paneth cell-specific	SS
107318	3	T74445	"yc82f8.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:2242 5', mRNA sequence"	Other
120983	3	AA398209	EST	Other
134700	3	AA481414	golgi SNAP receptor complex member 1	TM
131216	3	D31058	ESTs	SS
127565	3	D79516	"HUM272B04B Human aorta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-272B04 5', mRNA sequence."	Other
106882	2.9	AA489009	ESTs	Other
130874	2.9	T08287	ESTs	Other
101275	2.9	L37936	Ts translation elongation factor; mitochondrial	Other
111179	2.9	N67239	ESTs	Other
126086	2.9	H70975	"yr73g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:210960 5', mRNA sequence."	Other
105365	2.9	AA236275	ESTs	Other
118789	2.9	N75416	ESTs	Other
115117	2.9	AA256492	H.sapiens PAP mRNA	Other
100484	2.9	HG1103-HT1 103	"Guanine Nucleotide-Binding Protein Rai, Ras-Oncogene Related"	Other
101300	2.9	L40391	Homo sapiens (clone s153) mRNA fragment	Other
103075	2.9	X59543	ribonucleotide reductase M1 polypeptide	Other
132164	2.8	U84573	procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	Other
106716	2.8	AA464962	ESTs	Other
134098	2.8	X06323	Human MRL3 mRNA for ribosomal protein L3 homologue ( MRL3	Other
134485	2.8	X82153	cathepsin K (pseudodysostosis)	SS
129634	2.8	AA150726	ESTs	Other
112207	2.8	R49602	ESTs	Other
124904	2.8	R86970	ESTs	Other
125471	2.8	AA477571	UDP-glucose ceramide glucosyltransferase	SS
132180	2.8	AA405569	fibroblast activation protein; alpha	SS
104454	2.8	M84443	galactokinase 2	TM
134282	2.8	T25508	ESTs	Other
101558	2.8	M32011	neutrophil cytosolic factor 2 (85kD; chronic granulomatous disease; autosomal 2)	Other
130529	2.8	AA173238	small inducible cytokine A5 (RANTES)	Other
101804	2.7	M86699	TTK protein kinase	Other

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## FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
109565	2.7	F01930	ESTs	Other
112427	2.7	R62604	ESTs	Other
115188	2.7	AA261819	ESTs	Other
121831	2.7	AA425374	ESTs	Other
132454	2.7	W78726	ESTs; Highly similar to serine/threonine kinase [H.sapiens]	Other
116398	2.7	AA599729	Homo sapiens homeobox protein A10 (HOXA10) gene; complete cds	Other
100409	2.7	D86957	Human mRNA for KIAA0202 gene; partial cds	Other
130987	2.7	R45898	ESTs	Other
107217	2.7	D51095	ESTs	SS, TM
125698	2.6	AA748483	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene; partial cds; neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes; complete cds	SS
118722	2.6	N73563	ESTs	SS
104521	2.6	R11604	"y147c1.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:132 5', mRNA sequence"	Other
130800	2.6	AA223388	ESTs; Weakly similar to katanin p80 subunit [H.sapiens]	Other
134415	2.6	AA329274	protein tyrosine phosphatase type IVA; member 2	TM
116461	2.6	AA621557	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY IIIII [H.sapiens]	Other
100864	2.6	HG4297-HT4 567	Transcriptional Coactivator Pc4	Other
103818	2.6	AA150614	"z143h5.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:54729 5', mRNA sequence"	Other
105713	2.6	AA291321	ESTs	Other
114969	2.6	AA250775	ESTs	Other
130415	2.6	X07290	Human HF.12 gene mRNA	Other
101791	2.6	M83822	Human belge-like protein (BGL) mRNA; partial cds	Other
128131	2.6	A1283162	claudin 3	SS, TM
131564	2.6	AA491465	ESTs	Other
100279	2.6	D42084	Human mRNA for KIAA0094 gene; partial cds	Other
130149	2.6	J04031	methylenetetrahydrofolate dehydrogenase (NADP+ dependent); methanyletetrahydrofolate cyclohydrolase; formyletetrahydrofolate synthetase	Other
119688	2.6	W81710	ESTs	SS
126638	2.6	AA649257	ESTs	Other
131672	2.6	X12901	Human mRNA for villin	Other
134405	2.6	J04177	collagen; type XI; alpha 1	Other
101188	2.5	L20320	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	TM
104534	2.5	R22303	ESTs; Weakly similar to putative p150 [H.sapiens]	Other
135179	2.5	U43747	Friedreich ataxia	SS
124308	2.5	H93575	ESTs	SS
125621	2.5	A1051602	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	TM
101342	2.5	L76191	Interleukin-1 receptor-associated kinase 1	Other
129351	2.5	AA167268	ESTs	Other
103774	2.5	AA092898	ESTs; Weakly similar to R07G3.8 [C.elegans]	Other
131289	2.5	AA485697	ESTs	SS, TM
132094	2.5	W01996	ESTs; Highly similar to (define not available 4929683) [H.sapiens]	Other
103223	2.5	X74801	chaperonin containing TCP1; subunit 3 (gamma)	Other

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FIGURE 11 (CONT)  
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PRIMEKEY	Fold Upregulated In Tumors	Exemplar Accession	Complete Title	ORF Structural Info
105610	2.5	AA279991	ESTs	Other
115719	2.5	AA416997	ESTs	Other
134888	2.5	AA148094	Tat-Interacting protein (30kD)	Other
105564	2.5	AA262943	ESTs	Other
129689	2.5	AA130156	ESTs	Other
103391	2.5	X94453	pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)	Other
104182	2.5	AA479990	ESTs; Weakly similar to glioma amplified on chromosome 1 protein [H.sapiens]	SS, TM
123494	2.5	AA599786	ESTs	Other
122905	2.5	AA470070	ESTs	Other
109175	2.5	AA180496	ESTs	Other
129907	2.5	D80170	ESTs	Other
115142	2.4	AA258116	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Other
125474	2.4	AA151216	Homo sapiens 14-3-3 protein mRNA; complete cds	SS
125745	2.4	A1283493	ribophorin II	Other
100103	2.4	AF007875	dolichyl-phosphate mannosyltransferase polypeptide 1; catalytic subunit	Other
102687	2.4	U73379	Human cyclin-selective ubiquitin carrier protein mRNA; complete cds	Other
133170	2.4	U21049	epithelial protein up-regulated in carcinoma	SS, TM
109141	2.4	AA176428	ESTs	Other
132811	2.4	U25435	transcriptional repressor	Other
102862	2.4	X01057	Interleukin 2 receptor, alpha	SS, TM
104300	2.4	D37933	syntaxin 1B	Other
105091	2.4	AA148859	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	Other
110674	2.4	H89315	*yw25e09.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253288 3' mRNA sequence.*	TM
122571	2.4	AA452600	EST	Other
123421	2.4	AA598440	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	Other
132181	2.4	AA046939	ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	Other
129445	2.4	AA306121	ESTs	SS
113923	2.4	W80763	ESTs; Moderately similar to FK506-binding protein 65kD [M.musculus]	Other
100598	2.4	HG2463-HT2 559	Guanine Nucleotide-Binding Protein G25k	Other
130869	2.4	AA128100	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	Other
132393	2.4	W85888	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Other
100830	2.4	HG4074-HT4 344	Rad2	Other
133785	2.4	D21255	cadherin 11 (OB-cadherin; osteoblast)	SS, TM
100867	2.4	HG4316-HT4 586	Transketolase-Like Protein	Other
119859	2.4	W80702	ESTs	Other
135269	2.4	M77698	YY1 transcription factor	Other
115140	2.4	AA258030	ESTs; Weakly similar to (define not available 3874821) [C.elegans]	Other
102162	2.4	U18291	CDC16 (cell division cycle 16; S. cerevisiae; homolog)	Other

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FIGURE 11 (CONT)  
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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
100372	2.4	D79997	KIAA0175 gene product	TM
106981	2.4	AA521157	ESTs	Other
130114	2.4	AA234717	ESTs	Other
118129	2.3	AA459956	ESTs	Other
122235	2.3	AA438475	ESTs	Other
107315	2.3	T62771	Homo sapiens nucleoplasmn-3 (NPM3) mRNA; complete cds	SS
125905	2.3	T69868	chaperonin containing TCP1; subunit 2 (beta)	Other
133061	2.3	AB000584	prostate differentiation factor	SS
107531	2.3	Y13936	protein phosphatase 1G (formerly 2C); magnesium-dependent; gamma isoform	Other
125820	2.3	AA730136	teratocarcinoma-derived growth factor 1	Other
131725	2.3	AA456264	ESTs; Highly similar to (define not available 4176448) [H.sapiens]	Other
101228	2.3	L27706	chaperonin containing TCP1; subunit 6A (zeta 1)	Other
132571	2.3	R84594	ESTs; Highly similar to (define not available 4809026) [H.sapiens]	SS, TM
100090	2.3	AC002486	"Human BAC clone RG367O17 from 7p15-p21, complete sequence [Homo sapiens]"	Other
103658	2.3	Z74615	collagen; type I; alpha 1	SS, TM
104897	2.3	AA054641	ESTs	Other
106818	2.3	AA480890	ESTs	Other
113077	2.3	T40442	ESTs	SS
128773	2.3	M28879	granzyme B (granzyme 2; cytotoxic T-lymphocyte-associated serine esterase 1)	SS
129506	2.3	AA258286	Homo sapiens mRNA for KIAA0877 protein; partial cds	TM
133746	2.3	U44378	MAD (mothers against decapentaplegic; Drosophila) homolog 4	Other
134272	2.3	X76040	Lon protease-like protein	Other
106267	2.3	AA431873	Homo sapiens clone 24711 mRNA sequence	Other
133493	2.3	AA284143	Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA) mRNA; complete cds	Other
104278	2.3	C02582	ESTs; Highly similar to (define not available 5114045) [H.sapiens]	Other
127211	2.3	AA480935	"aa28c03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814564 5' mRNA sequence."	Other
110721	2.3	H97678	ESTs	Other
114774	2.3	AA150043	ESTs	TM
132968	2.3	N77151	Homo sapiens mRNA for KIAA0799 protein; partial cds	Other
106916	2.3	AA480814	ESTs	Other
113849	2.3	W60439	ESTs; Moderately similar to cbp146 [M.musculus]	Other
131028	2.3	U20240	CCAAT/enhancer binding protein (C/EBP); gamma	Other
130380	2.3	U55853	Homo sapiens 130 kD Golgi-localized phosphoprotein (GPP130) mRNA; complete cds	SS
125390	2.3	H95094	KIAA0016 gene product	SS, TM
127256	2.3	AA327550	ESTs; Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Other
132116	2.3	AA234767	ESTs	SS, TM
117765	2.3	N47797	ESTs	Other
119126	2.3	R45175	ESTs	Other
129482	2.2	AA435849	ESTs; Moderately similar to unknown protein [H.sapiens]	Other
120493	2.2	AA255933	ESTs	SS
108927	2.2	AA143493	ESTs; Weakly similar to PLECKSTRIN [H.sapiens]	Other

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## FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
122520	2.2	AA449427	ESTs; Moderately similar to pregnancy-specific beta-1 glycoprotein 2 [H.sapiens]	Other
125982	2.2	R98091	RAE1 (RNA export 1; S.pombe) homolog	Other
132325	2.2	N37065	ESTs; Moderately similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	Other
100287	2.2	D43950	Human mRNA for KIAA0098 gene; partial cds	Other
114895	2.2	AA236177	Homo sapiens mRNA for KIAA0887 protein; partial cds	Other
105038	2.2	AA130273	ESTs; Weakly similar to (define not available 4240269) [H.sapiens]	Other
105476	2.2	AA255473	ESTs	SS
106942	2.2	AA496347	ESTs; Highly similar to gene 7442 protein [H.sapiens]	Other
110566	2.2	H59990	ESTs	Other
111068	2.2	N58397	ESTs	Other
127983	2.2	AI299013	*qn13h12.x1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1898183 3' similar to TR:022813 O22813 PUTATIVE NAD(P)-DEPENDENT CHOLESTEROL DEHYDROGENASE. mRNA sequence.*	TM
130985	2.2	AA243700	ESTs	Other
132877	2.2	R40685	Homo sapiens mRNA for KIAA0851 protein; complete cds	TM
135242	2.2	M74093	cyclin E1	TM
129468	2.2	J03040	secreted protein; acidic; cysteine-rich (osteonectin)	SS
132616	2.2	AA386264	ESTs	SS, TM
133760	2.2	M14219	decorin	Other
121853	2.2	AA425887	ESTs	Other
114608	2.2	AA079381	ESTs	Other
128017	2.2	H13108	ESTs	SS
132725	2.2	L41887	splicing factor; arginine/serine-rich 7 (35kD)	Other
125606	2.2	R28463	ESTs	SS
105538	2.2	AA258860	ESTs; Highly similar to (define not available 4583654) [H.sapiens]	Other
133221	2.2	AA235289	ESTs; Highly similar to rap2 gene product [H.sapiens]	Other
105389	2.2	AA446949	ESTs	Other
128949	2.2	AA190993	a disintegrin and metalloproteinase domain 12 (meltrin alpha)	Other
120969	2.2	AA398116	ESTs	Other
102495	2.2	U51240	Human mRNA for KIAA0085 gene; partial cds	TM
101124	2.2	L10343	protease inhibitor 3; skin-derived (SKALP)	SS
102778	2.2	U83463	syndecan binding protein (syntenin)	Other
107307	2.2	T52099	creatine kinase; mitochondrial 2 (sarcomeric)	Other
111605	2.2	R11638	ESTs	Other
101959	2.2	S80343	arghlyl-tRNA synthetase	Other
101031	2.2	J05070	matrix metalloproteinase 9 (gelatinase B; 92kD gelatinase; 92kD type IV collagenase)	SS
131701	2.2	AA149008	ESTs; Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	Other
105344	2.2	AA235303	ESTs	TM
103166	2.2	X67951	proliferation-associated gene A (natural killer-enhancing factor A)	Other
131483	2.2	X74142	forkhead (Drosophila)-like 1	Other
131412	2.2	U34044	Human selenium donor protein (selD) mRNA; complete cds	Other
134982	2.2	N46086	ESTs	Other
127236	2.1	AI341818	budding uninhibited by benzimidazoles 1 (yeast homolog)	Other
104459	2.1	M91493	EST	Other

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FIGURE 11 (CONT)  
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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
124596	2.1	N70088	ESTs	Other
105650	2.1	AA282347	ESTs; Highly similar to (define not available 4454694) [H.sapiens]	Other
134917	2.1	X87241	FAT tumor suppressor (Drosophila) homolog	SS
132478	2.1	H20906	Homo sapiens mRNA for KIAA0748 protein; partial cds	SS, TM
134464	2.1	N79354	ESTs; Weakly similar to Rga [D.melanogaster]	Other
111221	2.1	N88869	ESTs	Other
		HG4557-HT4		
100892	2.1	962	"Small Nuclear Ribonucleoprotein U1, 1snrp"	Other
117170	2.1	H98153	ESTs	Other
124049	2.1	F10523	primase; polypeptide 2A (58kD)	Other
131692	2.1	D50914	Human mRNA for KIAA0124 gene; partial cds	TM
103003	2.1	X52003	trefoil factor 1 (breast cancer; estrogen-inducible sequence expressed in)	SS
134085	2.1	U20979	chromatin assembly factor I (150 kDa)	Other
126216	2.1	N23870	ESTs	Other
102721	2.1	U79241	Human clone 23759 mRNA; partial cds	Other
128040	2.1	AA918528	ESTs	Other
101038	2.1	J05249	replication protein A2 (32kD)	SS
106060	2.1	AA417287	C-terminal binding protein 2	Other
103622	2.1	Z48042	basic transcription factor 3	Other
127884	2.1	AA768630	ESTs	Other
130911	2.1	W72906	HIRA interacting protein 4 (dnaJ-like)	Other
104260	2.1	AF008192	Homo sapiens putative GR6 protein (GR6) mRNA; complete cds	Other
120714	2.1	AA292689	ESTs	Other
101578	2.1	M34423	galactosidase; beta 1	SS
113443	2.1	T86158	ESTs	SS
101518	2.1	M28249	Accession not listed in Genbank	Other
			ESTs; Moderately similar to IIII ALU SUBFAMILY SB WARNING ENTRY	
106480	2.1	AA450373	IIII [H.sapiens]	Other
111365	2.1	N92659	ESTs	Other
121121	2.1	AA399371	ESTs; Weakly similar to (define not available 4688925) [H.sapiens]	Other
124768	2.1	R40177	ESTs	Other
102501	2.1	U51586	Human slah binding protein 1 (SlahBP1) mRNA; partial cds	Other
106432	2.1	AA448850	ESTs	Other
132812	2.1	R48108	ESTs	Other
125681	2.1	AA394176	accessory proteins BAP31/BAP29	TM
130511	2.1	L32137	cartilage oligomeric matrix protein	Other
128219	2.1	AA978333	ESTs	Other
130962	2.1	AA102051	transmembrane 4 superfamily member 6	SS, TM
101840	2.1	M93056	protease inhibitor 2 (anti-elastase); monocyte/neutrophil	TM
123928	2.1	AA621363	EST	Other
			ESTs; Moderately similar to IIII ALU SUBFAMILY SC WARNING ENTRY	
132073	2.1	N67408	IIII [H.sapiens]	Other
101671	2.1	M61832	S-adenosylhomocysteine hydrolase	Other
107059	2.1	AA608545	ESTs	Other
132791	2.1	AA446088	ESTs; Weakly similar to YY1-associated factor 2 [H.sapiens]	Other
103131	2.1	X85614	S100 calcium-binding protein P	Other
104791	2.1	AA029046	ESTs	Other

## FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
135181	2.1	AA621349	ESTs; Weakly similar to similar to Yeast hypothetical protein L8167.12 like [C.elegans]	Other
104334	2.1	D82614	ESTs	Other
132103	2.1	AA025086	ESTs	Other
126743	2.1	AA179253	poly(A)-binding protein-like 1	Other
100439	2.1	D87453	Human mRNA for KIAA0264 gene; partial cds	Other
114860	2.1	AA235112	ESTs; Moderately similar to similar to murine RNA-binding protein [H.sapiens]	Other
116732	2.1	F13779	ESTs; Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	Other
131045	2.1	H30863	ESTs; Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster ring canal protein. [H.sapiens]	Other
133209	2.1	AA114183	ESTs; Moderately similar to glutamate pyruvate transaminase [H.sapiens]	Other
101758	2.1	M77836	Human pyrroline 5-carboxylate reductase mRNA; complete cds	Other
102214	2.1	U23752	SRY (sex-determining region Y)-box 11	Other
130100	2.1	AA425593	ESTs	Other
109799	2.1	F10770	Homo sapiens clone 669 unknown mRNA; complete sequence	Other
130860	2.1	U66061	T-cell receptor; beta cluster	SS, TM
106685	2.1	AA461551	ESTs; Highly similar to 73 kDa subunit of cleavage and polyadenylation specificity factor [H.sapiens]	TM
125724	2.1	AA083407	stimulated trans-acting factor (50 kDa)	Other
134258	2.1	L28010	heterogeneous nuclear ribonucleoprotein F	Other
129642	2.1	R50008	7-dehydrocholesterol reductase	TM
125336	2.1	T66823	ESTs	Other
125303	2	Z39821	ESTs	Other
100749	2	HG3521-HT3 715	Ras-Related Protein Rap1b	Other
126185	2	A1393989	ESTs	TM
126880	2	A1151406	ESTs	SS, TM
105263	2	AA227926	ESTs	Other
123288	2	AA495836	EST	Other
105807	2	AA393803	ESTs	Other
105040	2	AA131047	KIAA0698 gene product	TM
131977	2	F09788	procollagen-proline; 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase); alpha polypeptide II	SS
117992	2	N52000	ESTs	SS, TM
134037	2	X53586	Human mRNA for Integrin alpha 6	SS
132744	2	X54326	glutamyl-prolyl-tRNA synthetase	Other
101581	2	M34996	"Human MHC cell surface glycoprotein (HLA-DQA) mRNA, 3'end"	SS, TM
103576	2	Z26317	desmoglein 2	SS
131235	2	AA223284	ESTs; Moderately similar to (define not available 4680395) [H.sapiens]	Other
127910	2	AA781881	ESTs; Weakly similar to sperm fertilization protein sp56 precursor [M.musculus]	SS
101552	2	M31642	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	Other
106318	2	AA436570	Homo sapiens mRNA for pre-mRNA cleavage factor I subunit	Other
101192	2	L20859	Human leukemia virus receptor 1 (GLVR1) mRNA; complete cds	TM
104592	2	R81003	Homo sapiens serine protease mRNA; complete cds	SS
129095	2	L12350	thrombospondin 2	SS

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FIGURE 11 (CONT)  
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PRIMEKEY	Fold Upregulated In Tumors	Exemplar Accession	Complete Title	ORF Structural Info
105705	2	AA290767	ESTs	Other
128461	2	M63262	arachidonate 5-lipoxygenase-activating protein	SS, TM

Entry Key	Similarity	Accession	Sequence	Structural Info
16074	>10	AA001507	ESTs	other
25047	>10	AA011031	ESTs	other
25082	>10	AA017257	ESTs	other
16490	>10	AA026418	ESTs	other
25179	>10	AA031268	H.sapiens mR	other
25215	>10	AA035540	APOLIPOPRO	other
25282	>10	AA044825	ESTs	other
16810	>10	AA053636	ESTs	other
16835	>10	AA054438	ESTs	SS,
10747	>10	AA055841	ESTs	other
10748	>10	AA055892	ESTs	other
16993	>10	AA065300	Human mRNA	other
17051	>10	AA070801	ESTs	TM
10840	>10	AA084104	ESTs	other
7296	>10	AA085661	ESTs	other
7325	>10	AA090842	ESTs Weakly	other
17419	>10	AA113349	EST	?
17541	>10	AA127459	ESTs	other
17559	>10	AA128407	ESTs	other
25689	>10	AA128978	ESTs	?
17600	>10	AA130596	ESTs	other
10992	>10	AA132523	Homo sapiens	other
17654	>10	AA133250	ESTs	TM
17734	>10	AA137246	ESTs	other
25801	>10	AA148530	EST - RC_AA	TM
25806	>10	AA149007	EST	?
11121	>10	AA158359	Human TAR D	?
11160	>10	AA164289	ESTs	other
25925	>10	AA164494	ESTs Weakly	other
25934	>10	AA165355	Human clone	?
17987	>10	AA169379	ESTs	other
18008	>10	AA171895	Homo sapiens	TM
33953	>10	AA173290	Human HOXA	other
33980	>10	AA180223	CAMP-DEPEN	other
34013	>10	AA190888	EST - RC_AA	other
34014	>10	AA191348	ESTs	other
34015	>10	AA191353	ESTs	TM
34070	>10	AA196549	ESTs	other
18260	>10	AA206801	ESTs	?
34105	>10	AA207123	ESTs	SS,
34107	>10	AA209469	ESTs	other
18330	>10	AA216722	Human mRNA	TM
18362	>10	AA223912	Ribonuclease	other
18392	>10	AA227751	ESTs	SS,
34188	>10	AA228030	ESTs	TM
34197	>10	AA232315	Homo sapiens	other
25948	>10	AA234365	Homo sapiens	?
25951	>10	AA234556	EST	?
11581	>10	AA236533	Evi-1	other
26059	>10	AA236685	ESTs	other
26100	>10	AA242835	Human mRNA	other
11603	>10	AA243052	ESTs Highly	other
7785	>10	AA243375	EST - AA2433	other
34372	>10	AA251973	ESTs	?
26240	>10	AA252282	Human mRNA	TM

FIGURE 12

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34382	>10	AA252512	ESTs	other
34391	>10	AA252703	EST - RC_AA	other
26274	>10	AA253011	ESTs	?
34400	>10	AA253400	ESTs	other
26291	>10	AA253422	ESTs	?
26355	>10	AA256379	ESTs	other
11813	>10	AA258158	ESTs	other
34518	>10	AA278721	ESTs	?
26545	>10	AA278979	ESTs	other
26574	>10	AA279504	ESTs	other
34554	>10	AA280018	DNA polymera	other
34561	>10	AA280298	ESTs	TM
26628	>10	AA280641	ESTs Highly	TM
11869	>10	AA280670	ESTs	SS,
34575	>10	AA280738	ESTs	TM
26677	>10	AA281638	ESTs	?
26700	>10	AA282197	EST	?
34672	>10	AA284372	ESTs	other
34692	>10	AA285079	ESTs	other
12143	>10	AA290991	ESTs	other
8092	>10	AA316272	ESTs	TM
34904	>10	AA321746	EST	other
8111	>10	AA323787	ESTs	other
8125	>10	AA330771	Human protein	TM
26916	>10	AA331393	ESTs	other
26926	>10	AA342402	ESTs	other
26935	>10	AA347193	ESTs Weakly	TM
35038	>10	AA350541	ESTs Modera	TM
35049	>10	AA350857	ESTs	other
35106	>10	AA371561	EST Weakly s	?
35197	>10	AA398120	ESTs	other
35277	>10	AA398536	ESTs	other
35309	>10	AA398660	EST	other
35322	>10	AA398710	H. sapiens RM	TM
27037	>10	AA400198	ESTs	TM
35495	>10	AA400527	ESTs	?
27046	>10	AA400670	Homo sapiens	other
35500	>10	AA400715	ESTs	other
12480	>10	AA403116	Homo sapiens	other
35693	>10	AA405485	ESTs Weakly	other
35697	>10	AA405512	ESTs	other
35766	>10	AA406169	Homo sapiens	other
35769	>10	AA406206	ESTs	other
35798	>10	AA410231	ESTs	other
35801	>10	AA410291	ESTs	other
35803	>10	AA410295	ESTs	other
35822	>10	AA411144	ESTs	TM
35874	>10	AA412024	EST	?
35958	>10	AA412550	ESTs	other
36052	>10	AA417027	EST	TM
36258	>10	AA423962	ESTs Weakly	other
36288	>10	AA424502	ESTs	other
36307	>10	AA424803	EST	?
36371	>10	AA426017	ESTs	TM
36395	>10	AA426353	ESTs	other
38405	>10	AA426406	Homo sapiens	other

**FIGURE 12**  
(cont.)

38506	>10	AA429610	ESTs	other
38571	>10	AA430726	EST - RC_AA	SS,
38695	>10	AA433910	ESTs	other
38739	>10	AA435610	EST - RC_AA	?
38753	>10	AA435688	ESTs	other
38845	>10	AA436198	ESTs	?
13136	>10	AA436560	ESTs	SS,TM
13143	>10	AA436619	ESTs	SS,
36958	>10	AA442060	ESTs	other
36962	>10	AA442082	ESTs	?
36981	>10	AA442845	EST	?
13237	>10	AA443971	ESTs Weakly	?
13242	>10	AA445994	ESTs	other
37057	>10	AA446131	ESTs	other
37068	>10	AA446312	ESTs Weakly	other
37074	>10	AA446344	ESTs	SS,
37084	>10	AA446486	Homo sapiens	?
37135	>10	AA447540	EST	?
37159	>10	AA447714	EST - RC_AA	other
37168	>10	AA447772	ESTs	?
37246	>10	AA449311	Homo sapiens	other
37310	>10	AA451707	ESTs	other
37453	>10	AA454610	ESTs	?
37456	>10	AA454632	ESTs	TM
27787	>10	AA454660	ESTs	?
37492	>10	AA455248	EST - RC_AA	other
37546	>10	AA456641	ESTs	TM
37601	>10	AA458864	ESTs	other
37611	>10	AA458996	Human signal	SS,TM
37615	>10	AA459101	Human serine	other
37653	>10	AA460017	ESTs	other
37677	>10	AA460530	Homo sapiens	other
37777	>10	AA464860	Homo sapiens	other
8648	>10	AA465016	Homo sapiens	?
37816	>10	AA469954	EST	?
37829	>10	AA470084	ESTs	other
28015	>10	AA477421	ESTs	other
37978	>10	AA479294	EST - RC_AA	other
37979	>10	AA479295	ESTs Highly	other
37983	>10	AA479348	H.sapiens mR	other
14054	>10	AA485223	ESTs	TM
38121	>10	AA485724	EST - RC_AA	other
28122	>10	AA485928	ESTs Weakly	other
38167	>10	AA487207	EST - RC_AA	other
38172	>10	AA487424	EST - RC_AA	other
38179	>10	AA487492	Homo sapiens	other
38182	>10	AA487501	ESTs	other
38194	>10	AA487969	ESTs	other
28141	>10	AA488432	ESTs	?
38211	>10	AA488687	ESTs	other
38235	>10	AA489030	ESTs	other
38280	>10	AA489791	EST - RC_AA	other
38316	>10	AA490500	Homo sapiens	other
38330	>10	AA490882	ESTs	other
38456	>10	AA504343	ESTs	SS,
38460	>10	AA504462	ESTs	other

**FIGURE 12**  
**(cont.)**

38553	>10	AA521471	ESTs	other
38580	>10	AA598545	ESTs	?
38590	>10	AA598648	Human mRNA	other
38601	>10	AA598738	ESTs	?
28323	>10	AA599639	ESTs	other
38828	>10	AA609177	ESTs	TM
38838	>10	AA609215	EST - RC_AA	?
38867	>10	AA609318	Human cbl-b m	TM
38871	>10	AA609333	EST	?
38970	>10	AA609749	ESTs	other
38984	>10	AA609839	ESTs Modera	?
39045	>10	AA610077	ESTs	other
39062	>10	AA620333	EST	?
39080	>10	AA620552	EST - RC_AA	?
39110	>10	AA620709	ESTs Weakly	other
39176	>10	AA621091	ESTs	other
39218	>10	AA621330	ESTs	other
39221	>10	AA621346	Homo sapiens	other
39232	>10	AA621409	ESTs	other
21	>10	AB000905	H.sapiens hist	?
8903	>10	AFFX-HUMTF	AFFX-HUMTF	?
33890	>10	AFFX-HUMTF	AFFX-HUMTF	?
39302	>10	C14944	ESTs	other
39329	>10	C20797	EST	?
28644	>10	D12163	ESTs	other
218	>10	D13540	PROTEIN-TYR	other
236	>10	D13645	Human mRNA	other
9127	>10	D30037	PHOSPHATID	other
459	>10	D38293	Human mRNA	TM
39405	>10	D50975	ESTs	other
39433	>10	D52037	Human thymid	other
39436	>10	D52692	Human Ca2+	TM
14708	>10	D59388	EST	?
39488	>10	D60831	ESTs	other
39504	>10	D80632	ESTs	other
765	>10	D86096	Prostaglandin	?
787	>10	D86969	Human mRNA	other
789	>10	D86971	Human mRNA	other
39529	>10	F02202	ESTs	?
39535	>10	F02450	ESTs Modera	TM
18676	>10	F04022	ESTs	other
18718	>10	F04915	ESTs	other
18762	>10	F09458	ESTs	other
18782	>10	F09739	ESTs	other
29080	>10	F13655	ESTs Modera	other
19001	>10	H02890	ESTs	other
19164	>10	H10395	EST	?
39725	>10	H11323	ESTs	other
19203	>10	H11593	ESTs	other
19328	>10	H17808	ESTs	other
19387	>10	H20128	ESTs	?
39787	>10	H20131	ESTs	SS,
19389	>10	H20165	EST	?
39832	>10	H26279	EST - RC_H2	other
19591	>10	H40688	ESTs	other
29229	>10	H48459	Human mRNA	other

**FIGURE 12**  
(cont.)

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19727	>10	H52702	ESTs	?
19787	>10	H56679	ESTs	other
39995	>10	H62474	EST	SS, TM
29331	>10	H68116	ESTs	TM
29344	>10	H68839	EST	?
40064	>10	H72283	Human mRNA	other
40083	>10	H73466	MITOCHOND	other
19949	>10	H78263	ESTs	TM
40204	>10	H88296	EST - RC_H8	other
29523	>10	H88353	ESTs Weakly	?
29551	>10	H90134	ESTs	?
29645	>10	H95840	ESTs	?
20057	>10	H98079	ESTs	other
976	>10	HG2036-HT2	EST - HG2036	?
1158	>10	HG3344-HT3	EST - HG3344	?
1210	>10	HG37-HT37	EST - HG37-H	?
1346	>10	HG4716-HT5	EST - HG4716	?
1349	>10	HG4747-HT5	EST - HG4747	?
1445	>10	J03027	MHC class I p	?
1570	>10	K01383	EST - K01383	?
1684	>10	L07541	Replication fa	other
1852	>10	L17328	Human FE22	TM
1856	>10	L18920	MELANOMA-A	?
1863	>10	L19181	TRANSLATIO	other
2070	>10	L37378	Homo sapiens	SS, TM
2123	>10	L40396	Homo sapiens	other
2144	>10	L41349	Phospholipase	SS,
9723	>10	L44542	ESTs	other
2188	>10	L47276	EST - L47276	other
2343	>10	M15353	Eukaryotic tra	other
2627	>10	M29610	Glycophorin E	TM
2857	>10	M58597	Fucosyltransfe	TM
3021	>10	M68941	Protein tyrosin	other
3163	>10	M84424	Calhepsin E	?
3196	>10	M86917	Oxysterol bind	other
20088	>10	N20054	ESTs Weakly	?
29795	>10	N20641	ESTs Highly	other
40427	>10	N21147	ESTs	other
40444	>10	N22140	ESTs Highly	other
29893	>10	N23003	ESTs	TM
40498	>10	N26086	Homo sapiens	SS,
40559	>10	N33024	ESTs	SS,
30190	>10	N33264	EST	?
30207	>10	N33920	H.sapiens mF	other
20304	>10	N34686	Homo sapiens	?
20307	>10	N34830	ESTs	other
30265	>10	N35115	ESTs	other
40594	>10	N35388	ESTs	other
40604	>10	N38893	Homo sapiens	other
40631	>10	N45124	ESTs	other
40660	>10	N49104	NUCLEAR FA	other
30610	>10	N50138	EST	?
30617	>10	N50646	ESTs	other
30631	>10	N50807	EST	?
30790	>10	N52935	EST	?
20564	>10	N55443	ESTs	TM

## FIGURE 12 (cont.)

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40760	>10	N57927	ESTs Weakly	other
30938	>10	N58561	Cathepsin B	other
20814	>10	N59230	ESTs	SS,
20657	>10	N62889	ESTs	other
31136	>10	N63512	ESTs Weakly	TM
40827	>10	N64051	Homo sapiens	other
31310	>10	N66831	EST	?
40876	>10	N67607	Human Rho-a	other
20791	>10	N68057	Homo sapiens	?
40905	>10	N68738	ESTs	other
40911	>10	N69114	H.sapiens mR	other
40913	>10	N69218	ESTs	other
31484	>10	N69466	ESTs	other
31619	>10	N73449	ESTs	other
41005	>10	N79516	ESTs	TM
31818	>10	N89774	Homo sapiens	other
31872	>10	N91109	EST	other
41040	>10	N91948	ESTs	other
31944	>10	N93193	ESTs	other
41065	>10	N93618	ESTs	other
32034	>10	N98926	ESTs Modera	other
41107	>10	R01634	ESTs	other
41163	>10	R08176	ESTs	other
21238	>10	R08564	Plasminogen	other
21240	>10	R08613	ESTs	other
21412	>10	R20670	ESTs	other
21519	>10	R27975	EST - RC_R2	other
41381	>10	R42278	H.sapiens mR	?
32189	>10	R43183	ESTs	TM
32195	>10	R43471	ESTs Weakly	other
21902	>10	R43822	EST	?
21946	>10	R44707	ESTs	TM
22072	>10	R49406	ESTs	?
32240	>10	R50976	Ribonuclease	other
32258	>10	R55623	ESTs	other
22258	>10	R56432	ESTs	other
22282	>10	R59197	ESTs	other
32277	>10	R61493	Human mRNA	other
22372	>10	R62831	EST	?
22400	>10	R64109	ESTs	other
41593	>10	R64129	ESTs	other
10233	>10	R71427	ESTs Highly	other
41654	>10	R76437	THROMBOXA	TM
22557	>10	R76722	ESTs	other
22576	>10	R79111	ESTs	other
22593	>10	R79777	EST	?
41678	>10	R80675	EST	?
41719	>10	R89260	EST - RC_R8	other
22793	>10	R96208	ESTs	other
41752	>10	R97063	ESTs	other
3375	>10	S50223	HKR-T1	other
3406	>10	S66896	SQUAMOUS	other
3522	>10	S80267	Spleen tyrosin	other
41793	>10	T03887	ESTs	?
23198	>10	T40530	ESTs Weakly	other
23360	>10	T58531	ESTs	other

**FIGURE 12**  
**(cont.)**

32635	>10	T61116	ESTs	other
42177	>10	T79786	ESTs	?
23623	>10	T84047	ESTs	?
23662	>10	T86874	ESTs	other
42242	>10	T89579	Homo sapiens	other
23759	>10	T80313	ESTs	other
23832	>10	T92018	ESTs	other
32740	>10	T92950	ESTs	other
42290	>10	T95105	ESTs	?
3598	>10	U01157	Glucagon-like	SS, TM
3659	>10	U04313	Protease inhib	other
3799	>10	U10690	Human MAGE	?
3870	>10	U14518	Centromere p	other
3913	>10	U16261	Human MDA-M	SS,
4029	>10	U21090	Human DNA p	other
4157	>10	U28811	Human cyste	other
4178	>10	U30246	Human bume	TM
15006	>10	U30246	Human bume	TM
4193	>10	U31116	Human beta-s	TM
4306	>10	U36798	Homo sapiens	TM
4382	>10	U39817	Bloom syndro	other
4386	>10	U40622	DNA repair pr	other
4388	>10	U40714	Human tyrosy	other
4455	>10	U43944	MALATE OXID	other
4477	>10	U45880	Human IAP-lik	other
4680	>10	U55766	Human Rev ir	TM
4702	>10	U57341	EST - U5734	other
4713	>10	U57721	Human L-kynu	other
4787	>10	U61145	Human enhan	other
4862	>10	U65437	Human homep	?
4945	>10	U69108	Homo sapiens	other
4975	>10	U71088	Human MEK5	other
4994	>10	U72514	Human C2f m	other
5002	>10	U72761	Human karyop	other
5021	>10	U73524	Human putativ	TM
5149	>10	U79716	Human reelin	SS,
5214	>10	U83303	H. sapiens mR	?
5243	>10	U85946	Human brain s	other
32789	>10	W02779	ESTs Modera	other
42354	>10	W19346	ESTs	other
42390	>10	W40150	Homo sapiens	other
33006	>10	W46286	ESTs Weakly	TM
33020	>10	W46891	ESTs Weakly	other
33109	>10	W59961	Human mRNA	other
24197	>10	W67277	ESTs	other
24215	>10	W69425	ESTs	other
33301	>10	W73883	ESTs	other
33343	>10	W79834	ESTs Weakly	other
33377	>10	W81219	ESTs Weakly	other
42602	>10	W86423	ESTs	TM
33556	>10	W90705	Murine leukem	other
33616	>10	W93726	Protease Inhib	other
33666	>10	W95876	ESTs	TM
5510	>10	X05360	Cell division c	?
5558	>10	X07876	Wingless-type	SS,
5603	>10	X14253	Teratocarcino	TM

**FIGURE 12**  
(cont.)

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5619	>10	X14850	HISTONE H2A	SS,
5623	>10	X14975	T-CELL SURF	?
5692	>10	X17644	G1 to S phase	other
5789	>10	X54825	Matrix metallo	other
5799	>10	X55330	Aspartylglucos	SS,
5802	>10	X55544	CYCLIC-AMP	?
5857	>10	X58377	Human mRNA	other
5960	>10	X63575	ATPase Ca++	TM
5963	>10	X63629	Cadherin 3 (F	SS, TM
5986	>10	X64810	Proprotein con	?
6041	>10	X87155	MITOTIC KIN	other
6095	>10	X69962	Fragile X mer	other
6106	>10	X70683	SRY (sex dete	TM
6155	>10	X74331	DNA primase	other
6167	>10	X74887	Ribonuclease	other
6188	>10	X76029	NEUROMEDI	TM
6315	>10	X81889	H.sapiens mR	other
6382	>10	X85133	H.sapiens RB	other
6384	>10	X85137	Human kinesi	other
6438	>10	X89398	URACIL-DNA	?
6449	>10	X89986	H.sapiens mR	TM
6478	>10	X91648	H.sapiens mR	SS, TM
6479	>10	X91653	EST - X91653	?
6494	>10	X92689	H.sapiens mR	TM
6713	>10	Y08564	EST - Y08564	?
6790	>10	Y12394	Homo sapiens	other
24915	>10	YEL003w/	EST - YEL003	?
42773	>10	YEL019c/MM	EST - YEL019	?
24545	>10	Z38462	ESTs	other
33713	>10	Z39427	ESTs	other
33791	>10	Z40883	ESTs	other
42766	>10	Z99394	ESTs Moderat	other
21558	>10	R33112	Human AF-6 m	other
28718	>10	AA282576	ESTs	?
40113	.9955090946	H78003	ESTs	?
10801	.9879448276	AA069285	ESTs Weakly	other
37491	.9513600842	AA455239	ESTs Highly	other
23900	.9272347693	T95789	ESTs	other
254	.9198395324	O14657	Human mRNA	other
6885	.8970927914	Z29331	Ubiquitin-con	other
28693	.8850766398	H97819	ESTs	SS,
26482	.8765189024	AA262491	ESTs	other
23123	.8699502035	T25306	EST	?
26525	.8160399123	AA278392	ESTs	other
13110	.7643356603	AA435840	Homo sapiens	other
34863	.7087597628	AA299784	EST	other
39432	.7034550083	O51691	Phosphoribos	?
31312	.6513325388	N66845	ESTs Weakly	?
21112	.6358446348	R01179	ESTs	?
31572	.6254820694	N71294	ESTs	other
17903	.6221229758	AA160259	EST	?
20747	.6094813734	N66842	ESTs	other
4676	.9589223908	U55206	Homo sapiens	TM
34363	.5627081023	AA251587	Homo sapiens	other
39094	.9540788988	AA620636	ESTs	other
3888	.5372000133	U15128	Human beta-1	?

**FIGURE 12**  
**(cont.)**

39386	.9.506250529	D12184	ESTs	TM
7674	.4458059039	AA203742	ESTs	other
4182	.4329744134	U31099	Human DP pr	TM
4507	.9.422674945	U47050	Human putativ	TM
35606	.9.412026255	AA402227	ESTs Modera	other
4970	.3649551013	U70862	Human nuclea	?
19829	.3432151573	H58813	EST	?
14837	.2878584141	T40145	ESTs	TM
17336	.2822148675	AA099585	ESTs	other
40541	.2532836505	N30160	ESTs	other
29496	.2487643833	H85434	EST	?
29943	.1797074262	N24786	ESTs Modera	TM
17997	.1629681314	AA189633	EST	other
21320	.1243463318	R11673	ESTs	other
13883	.1178796537	AA476917	ESTs Weakly	other
30539	.0886887776	N49072	ESTs	other
32778	.0877919549	W02063	EST	?
28380	.0809559376	AA257012	EST	?
15888	.0595893607	X95632	Human Abl in	other
40812	.0012874244	N63419	ESTs	other
903	.9840387908	D90070	ATL-derived P	other
22674	.9515777733	R87160	ESTs	TM
40807	.9510132281	N62995	TRANSCRIPT	other
15244	.9195644974	W00904	ESTs	TM
32296	.8658776567	R67075	Zinc finger pro	other
18269	.8575656768	AA209467	ESTs	other
19662	.8507626284	H47391	ESTs	other
41607	.8.833925517	R67868	CLEAVAGE S	other
2548	.8299864695	M25897	Platelet factor	TM
7736	.8278341243	AA232121	Human tyrosy	other
34490	.7844537272	AA262354	ESTs	other
38658	.7669313482	AA599477	ESTs	other
7528	.8.765157554	AA149543	ESTs	other
39939	.7555031142	H53454	EST - RC_H5	other
25111	.7232692309	AA020787	ESTs	other
21655	.8.716167279	R38239	EST	?
39863	.8.665982852	H04756	ESTs Highly	other
1042	.8.652112324	HG2510-HT2	EST - HG2510	?
32330	.6361115426	R77776	ESTs	other
25382	.6239456487	AA059007	ESTs	other
27074	.5900813076	AA401475	ESTs Weakly	SS,
3955	.5298909183	U18259	MHC class II	other
4959	.8.52646827	U70322	Human transp	other
2315	.5259185808	M14123	EST - M14123	?
37253	.4896914632	AA449357	ESTs	other
39624	.8.471315877	F10836	ESTs	?
23213	.4569920887	T40891	ESTs	?
2798	.8.455596435	M54995	Connective tis	TM
41154	.4413390141	R07499	ESTs	?
32479	.4093689549	T18282	WEE1-LIKE P	other
41251	.3587565419	R28279	Human clone	other
19081	.3583603183	H06701	ESTs Weakly	other
21098	.3105927559	R00545	ESTs	other
14723	.3061679053	D59894	ESTs	other
37154	.2994822341	AA447666	Human CENP	other
8068	.2835585361	AA313387	ESTs Highly	other

**FIGURE 12**  
**(cont.)**

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7485	.8281679348	AA129547	ESTs	other
18501	.2517969834	AA026969	ESTs	other
34527	.2419183754	AA279091	ESTs	other
6700	.1948875662	Y07867	H.sapiens mR	other
2852	.1928816537	M58460	Human 75-kD	other
11188	.1882492468	AA172372	ESTs	TM
42293	.8.183311084	T95333	ESTs Weakly	TM
5443	.1763317544	X02530	Interferon (gam	SS,
40937	.1534810594	N70607	ESTs	TM
23371	.1499496068	T59505	EST - RC_T59	?
26272	.1339974518	AA252981	ESTs Weakly	other
17306	.1332403762	AA086201	ESTs	other
18497	.1192326373	AA233795	ESTs	other
235	.0944363901	D13644	Human mRNA	other
24525	.0860187097	Z38347	ESTs	TM
7826	.0750029554	AA248884	EST - AA2488	TM
32142	.0739258775	R38715	Homo sapiens	other
39067	.0557768803	AA620405	ESTs	other
6235	.0448957236	X78416	Casein alpha	TM
29517	.0017588729	H88261	ESTs	other
28570	.9852455973	C21104	Homo sapiens	other
39344	.9162087762	C21034	ESTs Moderat	other
18951	.9002189758	H00580	ESTs	other
18953	.8709160227	H00615	ESTs	other
18376	.8564099916	AA226925	ESTs	other
19830	.7847878447	H58911	ESTs	other
36023	.7840835828	AA416881	ESTs	other
13347	.8344414518	AA449238	ESTs	other
36614	.8284591351	AA431466	ESTs	other
2192	.8254072032	L48211	Homo Sapien	?
33016	.8006574068	W46577	H.sapiens mR	other
17215	.7941954038	AA083044	ESTs	other
34894	.7659738108	AA311881	EST	?
40614	.7695001222	N39257	ESTs	other
36295	.6834749899	AA424534	ESTs	other
19564	.6744302788	H38833	ESTs	TM
16914	.6686405336	AA058665	ESTs	SS,
35967	.6378078107	AA412694	Human splicin	other
21672	.6364823402	R38635	ESTs	other
19918	.6303275831	H69787	ESTs	?
10511	.6297744492	AA024482	ESTs Highly	other
17721	.6057811016	AA136590	ESTs	?
42302	.6031859692	T96130	EST	SS,
26134	.6000619383	AA243763	ESTs	other
18766	.5621799008	F09497	ESTs	other
34492	.7.501590494	AA262439	ATL-derived P	other
270	.4512152125	D14822	EST - D14822	other
35975	.4177746988	AA412738	ESTs	other
29842	.4095809671	N21688	ESTs	?
35389	.3913043318	AA399555	ESTs	other
19979	.3868157168	H88477	ESTs	other
5793	.3865864025	X54942	CDC28 protei	other
19978	.7.380969715	H87770	EST - RC_H8	other
1280	.3691089318	HG4126-HT4	EST - HG4126	?
31571	.3676263454	N71250	ESTs	other
23765	.3541191734	T90443	ESTs Weakly	?

**FIGURE 12**  
(cont.)

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35123	.3397933455	AA380927	EST	?
38252	.3341119467	AA489247	ESTs	other
38216	.3262021037	AA488861	ESTs	other
29418	.2489407009	H77915	EST - RC_H7	?
4834	.1980951054	U63541	Human mRNA	other
42504	.1913036522	W69803	ESTs	other
6111	7.158000198	X71125	H.sapiens mR	TM
41773	7.154479618	T03024	ESTs Weakly	other
9951	.1363626368	N71513	ESTs	other
28109	.0941968224	AA485212	ESTs	other
988	.0783044659	HG2160-HT2	EST - HG2160	?
29848	.0610668511	N22107	ESTs	other
30628	.0607950168	N50744	ESTs	other
22567	.0225726353	R77771	ESTs	TM
9347	7.006323071	H03686	ESTs	TM
11696	.0026773296	AA252894	ESTs	other
40584	.0010096333	N34870	EST	?
193	.9767029188	D10923	PROBABLE G	TM
18305	.9740536051	AA214048	Collagen type	other
6078	.9699682397	X69141	FARNESYL-D	other
26741	6.902658703	AA283198	ESTs	other
35069	.8992865685	AA358397	EST	?
23504	.8977135983	T71042	ESTs	other
299	.8824513029	D16815	Homo sapiens	other
40583	.8689903023	N34855	ESTs	other
31428	.8623762224	N68594	ESTs	other
6169	.8608959727	X75091	SET PROTEIN	other
39524	.8567355171	F01905	MALATE OXID	other
34578	.8430689439	AA280837	ESTs	other
38678	6.837527995	AA599920	Small inducib	other
23936	.8251471804	T96930	ESTs	other
9326	.8181321394	D89377	Msh (Drosoph	other
18188	.8067351968	H11255	ESTs Highly	TM
18185	.7882148811	AA194983	Homo sapiens	other
27028	6.757529124	AA399630	ESTs Weakly	other
41289	.7519531681	R37265	EST	other
34511	.7364448798	AA278298	EST - RC_AA	other
1566	.7056207716	J05614	EST - J05614	?
25675	.6692299748	AA129757	ESTs Highly	other
5814	.6584342828	X56088	CYTOCHROM	SS,
13861	.6236291607	AA470145	ESTs	other
29794	.6026313352	N20598	ESTs	other
39333	.5902382643	C20910	Cyclin B1	other
3770	.5835303599	U09609	Nuclear factor	other
31831	.5829933764	N89894	ESTs	?
33063	.5808125026	W53000	Homo sapiens	other
20326	.5640084836	N35583	ESTs Weakly	?
34384	.5535703492	AA252537	ESTs	other
25599	.5490481991	AA114091	Human (clone	other
39749	.5369363254	H14988	ESTs	other
42596	.5200567072	W85900	ESTs	?
39606	.5119482185	F10243	ESTs Weakly	?
14617	.5105504748	C14983	ESTs	other
27831	6.45670814	AA456044	ESTs	?
34896	.4496517783	AA312551	EST	?
27360	.4434305006	AA425356	ESTs	other

**FIGURE 12**  
**(cont.)**

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20126	.4326610424	N22015	ESTs	TM
6683	.4324809977	Y00291	RETINOIC AC	TM
30692	.4196836207	N51563	ESTs	other
36472	.4189542265	AA428633	EST	?
9578	.3961788753	H87652	Homo sapiens	other
39670	.3818496159	H05626	ESTs	other
22697	.3652792447	R89218	ESTs	other
37308	.3647804993	AA451694	EST	TM
16101	.3517262802	AA002147	EST	?
20629	.3486854401	N59798	ESTs	other
36100	.3364146287	AA417740	ESTs	?
15488	.3252590241	W28097	Homo sapiens	other
36867	.3131273544	AA432136	ESTs	other
30766	.3116037924	N52627	EST - RC_N5	?
32882	.2745311453	W37683	ESTs	TM
18072	.2675797205	AA180448	EST	?
18231	.2652604863	AA199747	Human mRNA	other
38282	.2514165676	AA489814	EST	?
28125	.6.250317021	AA486073	ESTs	other
37464	.2484456382	AA454747	ESTs	?
36618	.1946328223	AA431478	ESTs	other
5082	.1931116815	U78524	Human Gu bln	other
1441	.1777287039	J02963	Integrin alpha	other
42105	.6.14875944	T67710	ESTs	?
6061	.1394863141	X68314	Glutathione pe	SS,
32570	.1156028796	T30222	ESTs Weakly	TM
32504	.1019612076	T17063	EST	?
23335	.0977927504	T56804	EST	?
10867	.0970991075	AA088458	ESTs Weakly	other
30883	.0911993489	N56923	EST	?
14528	.0859008453	AA620295	ESTs	TM
29454	.0685955036	H81308	EST	?
6798	.0539173276	Y13153	Homo sapiens	TM
21248	.0525426545	R08871	ESTs	?
21940	.0499964136	R44538	ESTs	?
29066	.0455247653	F10927	Homo sapiens	other
18774	.0446826953	F09609	ESTs	?
36722	.0172343991	AA435512	ESTs	SS,
18062	.0034342969	AA179845	ESTs Modera	other
22989	.9992817406	T16305	ESTs	other
41745	.9905623898	R95895	ESTs	?
8787	.9894877656	AA504307	X-LINKED HE	other
20550	.5.984861795	N55013	ESTs	other
26470	.9417764101	AA262179	ESTs	other
16574	.9356497569	AA031926	EST	other
693	.9169537385	D80007	Human mRNA	other
4093	.5.914830973	U25182	Human antiox	TM
1192	.9086264407	HG3546-HT3	EST - HG3546	?
22956	.8954735623	T10248	ESTs	other
36723	.5.891606409	AA435524	EST	?
2114	.8844986595	L40384	EST - L40384	other
26872	.5.868236789	AA291137	ESTs	other
6602	.8663883018	X98286	EST - X98286	other
42701	.8594493433	Z38612	ESTs	other
28573	.5.84591116	C21118	ESTs	other
18290	.8189427595	AA211901	ESTs	other

**FIGURE 12**  
**(cont.)**

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732	.804391794	D83781	Human mRNA	other
5330	.801414561	U91327	EST - U91327	?
33503	.799071518	W88720	EST	?
2553	.779750586	M26167	Human platele	?
34705	.765880625	AA288907	ESTs Weakly	other
42665	.759409104	W93659	ESTs	other
38180	.753931079	AA487495	EST - RC_AA	other
4244	.747673880	U33286	Human chrom	other
32822	.741895745	W16834	ESTs	TM
3977	.724588555	U18991	Retinal pigme	?
24873	.720236615	Z39301	ESTs	TM
6928	.712026112	Z46829	SRY (sex-def)	other
38726	.703079625	AA608733	ESTs	?
39290	.689237205	C14573	Human mRNA	other
11405	.681887379	AA232231	ESTs	other
22538	.679200659	R73567	Homo sapiens	TM
40747	.660539320	N56872	Homo sapiens	TM
31596	.655402460	N72094	ESTs	other
6329	.641565251	X82279	EST - X82279	?
31578	.627332366	N71361	ESTs	other
33207	.627181848	W70051	H.sapiens mR	other
2545	.610586014	M25753	Cyclin B1	other
22580	.598840264	R79156	ESTs	other
33592	.593531451	W93127	ESTs	other
28843	.573469875	D60252	ESTs	other
6160	.568905061	X74794	CDC21 HOMO	other
37987	.556134567	AA479666	ESTs	other
42515	.521786861	W72116	Homo sapiens	other
4732	.513066852	U58522	Human huntin	other
3299	.509985067	M95623	Hydroxymethyl	?
28320	.547340698	AA589574	ESTs	?
746	.547126089	D84454	Human mRNA	TM
39373	.463580495	C21517	ESTs	other
3117	.439841353	M81182	Peroxisomal m	other
21257	.434361244	R09196	ESTs Modera	other
31487	.431864885	N69507	ESTs	other
28954	.413713051	F03153	ESTs	other
38928	.538978272	AA609595	ESTs	other
29903	.372232062	N23366	EST	?
30925	.343743231	N58295	ESTs Weakly	?
19091	.334461568	H07864	ESTs	TM
28209	.313895191	AA491250	ESTs	other
9470	.311889798	H46617	EST - H46617	other
9435	.307005665	H30201	EST - H30201	?
28552	.295443257	C20914	ESTs	other
27411	.294016426	AA428137	ESTs	other
30615	.282412526	N50556	ESTs	other
28313	.265797716	AA599309	ESTs	TM
39321	.264903538	C20632	ESTs	?
29834	.253104739	N24194	ESTs	other
1094	.249670312	HG2846-HT2	EST - HG2846	?
39578	.248112638	F08925	ESTs	TM
11232	.246679842	AA186804	ESTs Weakly	other
2466	.242634932	M21539	Human small	other
26843	.238775866	AA287450	ESTs	?
40331	.235338556	H97562	ESTs Weakly	other

**FIGURE 12**  
(cont.)



8035	5.205798365	AA305116	EST - AA305	other
29793	.195542572	N20593	ESTs Weakly	other
34109	.148159010	AA210722	EST	?
26408	.143257725	AA258177	ESTs Weakly	other
19263	.142702980	H15054	ESTs	TM
24596	.141608935	Z38810	ESTs	other
28589	.136505975	C21245	H.sapiens mF	other
5684	.112193141	X17098	Pregnancy-sp	other
30710	.107934734	N51761	EST	?
35765	.097351494	AA406167	EST	?
26360	.088312788	AA256480	ESTs	?
2351	.084961209	M15796	Proliferating c	?
30262	.083687753	N35065	Homo sapiens	other
41792	.073751246	T03886	ESTs	?
36710	.070383966	AA434411	ESTs	other
39090	.054688540	AA620628	ESTs	TM
42185	.053992638	T79951	ESTs	?
18745	.048032155	F09134	ESTs	other
35746	.039684199	AA406063	ESTs	other
35356	.035480958	AA399053	EST	?
36769	.031270687	AA435750	EST	?
36900	.027991154	AA436866	H.sapiens mF	other
27595	.024475730	AA443328	ESTs	TM
16290	.005661190	AA016145	ESTs	?
27117	.001614659	AA405098	ESTs Weakly	other
4304	.995195439	U36764	Eukaryotic tra	other
33458	.990740207	W86835	Homo sapiens	other
26893	.980009067	AA282120	EST	?
12669	.975813865	AA417030	Homo sapiens	other
29701	.970852638	H97970	EST	?
20480	.955725363	N52168	ESTs	TM
8720	.943911060	AA481218	EST - AA4812	other
34828	.943126947	AA292436	Homo sapiens	SS, TM
14985	.494162103	U15128	Human beta-	?
16115	.937755352	AA004420	ESTs	?
42506	.934858711	W70074	EST	other
34761	.931683744	AA287833	ESTs	other
11870	.928105620	AA262587	ESTs	TM
23211	.925839185	T40889	ESTs	other
40611	.916050227	N39138	Homo sapiens	other
42611	.912860535	W87006	Homo sapiens	other
39652	.904517460	H03099	ESTs	other
17581	.488967475	AA129395	EST	?
37239	.870437538	AA449121	ESTs	?
18712	.870361878	F04677	ESTs	other
30709	.881117195	N51752	ESTs Weakly	other
34179	.850361394	AA227903	ESTs Highly	other
21433	.482567098	R22183	EST	?
39731	.816614274	H11760	ESTs	other
31295	.811661480	N66653	ESTs	other
24647	.480416305	Z39108	EST	?
31292	.800887181	N66615	ESTs	other
1285	.799754239	HG4157-HT4	EST - HG415	?
1106	.793242585	HG2981-HT3	EST - HG298	?
18212	.791226256	AA196508	ESTs	other
34367	.478220704	AA251758	Homo sapiens	other

**FIGURE 12**  
**(cont.)**

34802	.7797760205	AA291468	ESTs	TM
34762	.7775301546	AA287834	ESTs	other
11595	.7696612848	AA242819	ESTs	other
8295	.7639839111	AA405082	ESTs	?
17622	.4758635576	AA131584	ESTs Weakly	other
35781	.7572463523	AA406335	ESTs	other
34754	.7483874972	AA287642	Human mRNA	other
23237	.7444854356	T47291	EST	?
37667	.7280445357	AA460318	ESTs Highly	other
11568	.7257189975	AA236786	ESTs	other
38622	.7190695733	AA598967	ESTs	?
5137	.7057359474	U79296	Dihydrolipoar	other
25038	.7002244728	AA010065	CDC28 protei	other
19288	.7000147312	H16567	ESTs	other
32503	.6979488292	T17045	Collagen type	other
3278	.6953739298	M94055	SODIUM CHA	TM
9696	.6942061018	L38961	Integral trans	TM
35400	.6901390896	AA399591	Homo sapiens	other
35246	.6862691303	AA398367	EST Weakly s	?
36387	.6822499271	AA426270	ESTs	other
21509	.6730072542	R27314	ESTs	other
31381	.6729672124	N67889	ESTs	other
26723	.6727894925	AA282781	ESTs Highly	other
36326	.6703621086	AA425151	Human GAP S	other
17409	.6688418667	AA113136	EST - RC_AA	other
4908	.6552339935	U87156	Human mitoge	other
30594	.6496238328	N49967	ESTs	other
38286	.646639735	AA489847	ESTs Weakly	?
13073	.6426509458	AA433950	ESTs	other
40435	.6240181068	N21614	Homo sapiens	other
14474	.6228694379	AA609427	ESTs Modera	other
38213	.615309907	AA488847	ESTs Weakly	?
5312	.606644198	U90716	Human cell st	SS, TM
24225	.6041550358	W70326	ESTs	?
35588	.5868982366	AA401750	EST	?
29739	.5863199051	H99826	EST	?
7203	.5792992577	AA053096	EST - AA0530	other
2157	.5772055869	L41939	Homo sapiens	SS, TM
32086	.5661024278	R11510	ESTs	?
8085	.5648114738	AA314779	ESTs Weakly	SS,
224	.5622018988	D13633	Human mRNA	other
34008	.5609980241	AA188761	DNA polymera	other
33656	.5557384389	W95477	ESTs	other
34065	.5537335124	AA195517	ESTs Weakly	TM
6028	.5357922097	X66503	Adenylosuccin	other
4166	.5032930671	U29463	Cytochrome B	?
40262	.5024727522	H93562	ESTs	TM
22687	.5018672549	R88209	ESTs	TM
41069	.4977510482	N93969	H.sapiens mR	SS,
8264	.4793100575	AA401334	ESTs	other
27588	.472017297	AA443187	ESTs	other
35882	.4717597552	AA412047	ESTs	?
34479	.4655519191	AA282080	Human burnet	TM
15921	.4548516436	Y12065	Homo sapiens	?
11279	.438003867	AA195399	ESTs	other
39222	.4367650786	AA621348	ESTs Highly	other

**FIGURE 12**  
(cont.)

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34428	.4364736768	AA256526	ESTs	other
8771	4.432067373	AA491188	ESTs	other
22193	.4189610024	R53891	Homo sapiens	other
7898	.4066170674	AA263032	ESTs	other
19902	.3886145805	H86736	ESTs	other
9276	.3868095206	D82374	ESTs	other
10716	.3794529068	AA053319	ESTs	TM
13183	.3751913512	AA442763	ESTs Highly	other
5690	.3723059417	X17620	NUCLEOSIDE	other
35102	4.37147138	AA371509	EST - RC_AA	TM
17983	.3612985467	AA169226	ESTs	other
24962	.3497206925	AFFX-HUMT	AFFX-HUMT	?
31680	.3416539669	N74438	ESTs	other
27168	4.330306894	AA410258	ESTs	other
28731	.3231846659	D20981	EST	?
28348	.3212284906	AA608752	ESTs	other
16335	.3019961487	AA018587	ESTs Weakly	?
33036	.2915644973	W48580	ESTs Weakly	other
30180	.2897721928	N33144	ESTs	other
35591	.2895541242	AA401758	ESTs Weakly	SS,
25340	.2721717135	AA054554	EST	?
28106	.2659103748	AA485084	ESTs	other
38690	.2649184307	AA800121	ESTs	other
20203	.2626499431	N28855	ESTs Modera	other
10251	.2608760694	R76185	ESTs Weakly	SS,
12684	.2604192389	AA417558	ESTs	SS,
31636	.2509469427	N73680	Natural resista	TM
20769	.2478765348	N67277	ESTs	other
1572	.2353281083	K01884	EST - K01884	?
10923	.2292322072	AA116036	ESTs	other
34380	.2283792392	AA252414	ESTs	other
10132	.2222816115	R35733	EST - R35733	other
16629	.2161752115	AA036811	ESTs	other
25146	.1969683794	AA026356	ESTs	?
28730	.1965943098	D20959	ESTs Modera	other
10200	.1874912391	R84521	ESTs	other
38695	.1545794663	AA600176	ESTs	other
31365	4.150549979	N67550	ESTs	other
42379	.1496120668	W37999	ESTs	other
28050	.1428703354	AA479139	Acid phosphat	other
2620	.1386565707	M29474	Human recom	?
8927	.1340593744	AF008442	Homo sapiens	other
13379	.1269549188	AA449741	ESTs Weakly	other
5134	.1218251808	U79293	Human clone	other
2626	4.1213948	M29581	Zinc finger pro	other
38005	.1160483666	AA479969	ESTs	other
36575	.1127196584	AA431085	EST	?
18296	.1121837207	AA213620	ESTs Weakly	?
29531	.1111459313	H88953	EST - RC_H8	TM
143	.1095880506	AFFX-HUMT	AFFX-HUMT	?
10970	.0967613396	AA129390	ESTs	other
25836	.0952825397	AA152305	Interferon (gam	SS,
19735	.0937927853	H53038	EST	?
40711	.0909709431	N53564	ESTs	other
4149	.0901471427	U28386	RAG (recomb	TM
5767	.0862784557	X53793	MULTIFUNCT	other

**FIGURE 12**  
(cont.)

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5503	.0861035825	X05232	Stromelysin	SS,
20310	.0641711656	N34893	ESTs Highly	other
456	.0599824566	D38145	Prostaglandin	SS,
7814	.0559885576	AA248406	ESTs	other
40230	.0447282719	H90161	ESTs	SS,
33651	4.039204804	W95409	ESTs	other
18777	.0231657926	AA046968	EST	?
19110	.0094905222	H08778	ESTs	other
34442	.0077010365	AA258093	HKR-T1	other
5099	4.004992433	U79247	Human clone	TM
8209	.9990473163	AA384220	ESTs	other
24408	.9976586074	W90146	ESTs	other
26596	.9974919787	AA279943	ESTs	other
16485	.9811264006	AA026269	Spleen focus	other
32969	.9804901745	W42451	ESTs	TM
27006	.9799768093	AA398695	ESTs Weakly	other
29809	.9526765967	N21043	EST	?
9596	.9440163451	H91564	ESTs	TM
29024	.9377933938	F09315	Homo sapiens	other
21894	.9356365584	R39317	Homo sapiens	other
13207	3.829998104	AA443321	ESTs	other
37865	.9143752626	AA476623	ESTs Highly	other
36201	.9129828172	AA421164	ESTs	?
8981	.8981160269	AFFX-HUMT	AFFX-HUMT	?
17444	.8927133917	AA115933	ESTs	other
25869	.8919834527	AA157267	ESTs Highly	TM
24862	3.89042252	Z41415	ESTs Highly	other
26685	3.889363206	AA281950	ESTs	?
42300	.8850230366	T95850	ESTs	?
6495	.8830844863	X92715	Zinc finger pro	other
38604	.8828045942	AA598803	ESTs	TM
36358	.8826713718	AA425756	ESTs	other
30560	3.873276445	N49284	MYB PROTO	other
14413	.8724466156	AA600150	ESTs	other
23823	.8574824967	T91805	Homo sapiens	other
38158	3.853096838	AA487021	EST	?
2572	.8519747554	M27281	Vascular endo	other
40100	.8464168967	H75933	Laminin recep	other
40258	.8462992993	H93340	ESTs	TM
20944	.8461621525	N74443	ESTs	other
20411	.8459400966	N48963	Homo sapiens	other
10345	.8457714481	AA001663	ESTs	other
31261	.8451974374	N66248	EST	other
8513	.8378410994	AA446990	ESTs	other
13877	.8363409835	AA476604	ESTs	other
40748	.8253562321	N56879	EST	?
14509	.8152852193	AA609943	ESTs	other
10281	.8065567331	R80333	ESTs	other
25284	.8044158642	AA045074	ESTs Weakly	other
6730	.7900025129	Y09305	H.sapiens mR	other
16033	.7884592402	AFFX-HUMIS	AFFX-HUMIS	?
39242	.7827184806	AA621523	ESTs	other
27354	.7794760435	AA425221	ESTs	?
4552	3.777263605	U49188	Human placen	SS, TM
18385	.7756199108	AA227219	Homo sapiens	other
16754	.7677416053	AA046067	EST - RC, AA	other

**FIGURE 12**  
**(cont.)**

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12752	.7671137403	AA421250	ESTs	other
42463	.7601033106	W60180	ESTs	other
10614	.7581669016	AA037357	ESTs	?
867	.7459337969	D87716	Human mRNA	other
7608	.7336047135	AA180967	ESTs	other
31795	.7327387421	N80703	ESTs	other
35377	.7273784603	AA399453	EST - RC_AA	?
22828	.7243928524	R98192	ESTs	other
25240	.7243198336	AA039713	ESTs	other
11008	.7197381366	AA134289	ESTs Weakly	?
4341	.7162349944	U38545	Human ARF-a	other
28833	.7147818393	D59787	EST - RC_DS	?
3750	.7121007154	U09279	Collagen type	SS,
17483	.6943413512	AA122147	ESTs	TM
16854	.6915208474	AA055552	ESTs Weakly	TM
3709	.6891656771	U07550	Heat shock 10	other
1608	.6652978422	L00205	KERATIN TYP	?
24577	.6617721053	Z38727	Homo sapiens	TM
31032	.6570916386	N62508	ESTs	other
4951	.6536195433	U69546	Human RNA b	other
37660	.6523275307	AA460225	ESTs	other
20418	.6495357091	N49209	ESTs	other
27995	.6485167436	AA470155	Homo sapiens	?
7971	.6434397185	AA287423	ESTs	other
27606	.64303453	AA443793	ESTs	other
24677	.6427250633	Z39338	ESTs Highly	other
11070	.6406198277	AA148521	ESTs Weakly	TM
9328	.6356048598	D89618	Homo sapiens	other
36826	.634689802	AA435996	ESTs	other
17678	.6300045795	AA134275	Human HIV1	other
36209	.6274694477	AA421266	ESTs Weakly	other
34120	.6258090412	AA211615	EST	?
38152	.6246442011	AA486737	H.sapiens mR	TM
38463	.6184693266	AA504491	ESTs Weakly	TM
20064	.6183699978	H98853	ESTs	TM
31256	.5992620732	N66152	EST	?
9713	.5985228843	L44338	Homo sapiens	other
28622	.5768056147	D11837	ESTs	?
38057	.5736105703	AA481549	EST - RC_AA	other
28763	.5688723791	D45568	EST	?
16996	.5680705708	AA069038	EST - RC_AA	TM
28628	.5604144617	D11888	ESTs Modera	?
25804	.5442954572	AA148885	ESTs	?
2492	.5423964239	M22898	Tumor protein	?
14904	.5411970737	T83389	ESTs Highly	other
25265	.5347588502	AA043765	H.sapiens RY	other
13606	.5327912417	AA456437	ESTs Weakly	other
42307	.5318436465	T96595	EST - RC_T96	TM
1544	.526202414	J05068	TRANSCOBA	SS,

**FIGURE 12**  
(cont.)

Accession	Gene	Protein	Accession	Gene	Protein
Accession	Gene	Protein	Accession	Gene	Protein
CZAB	111929	3.7	R40057	prominin (mouse)-like 1	
BCX2	128790	4.0	AA291725	secreted frizzled-related protein 4	
CBC2	101809	5.7	M80849	Homo sapiens connexin 26 (GJB2) mRNA, complete cds	
CBC1	100365	4.8	D78811	mesoderm specific transcript (mouse) homolog	
CBC3	102618	2.5	U65932	extracellular matrix protein 1	
	134804	6.3	L37036	small inducible cytokine subfamily B (Cys-X-Cys); member 5 (epithelial-derived neutrophil-activating peptide 78)	
	104209	2.1	AB000221	small inducible cytokine subfamily A (Cys-Cys); member 15; pulmonary and activation-regulated	
CJA8	115697	8.1	AA411502	ESTs; Weakly similar to airway trypsin-like protease [H.sapiens]	
	124315	5.4	H94892	viral simian leukemia viral oncogene homolog A (ras related)	
	109415	4.3	AA227219	Homo sapiens CAGF9 mRNA; partial cds	
	103813	5.1	Z46629	SRY (sex-determining region Y)-box 9 (campomelic dysplasia; autosomal sex-reversal)	
	109166	6.2	AA179845	RAB8 interacting; kinesin-like (rabkinesin6)	
CJA9	116176	5.7	AA463725	ESTs; Weakly similar to KIAA0226 [H.sapiens]	
CGA7	115522	8.1	AA331393	ESTs	
	125852	5.7	H09290	ESTs; Weakly similar to unknown [H.sapiens]	
BCN5	112244	3.1	R51309	ESTs	
CQA1	132892	5.6	AA129390	ESTs	
BCN7	117280	5.4	N22107	ESTs; Moderately similar to [H] ALU SUBFAMILY SC WARNING ENTRY [H] [H.sapiens]	
	102663	4.8	U70322	karyopherin (importin) beta 2	
CQA2	104660	6.0	AA007160	ESTs	
	113702	2.4	T97307	ESTs; Moderately similar to [H] ALU SUBFAMILY J WARNING ENTRY [H] [H.sapiens]	
	100154	6.0	D14657	KIAA0101 gene product	
	102260	3.7	U28396	Human nuclear localization sequence receptor hSRP1alpha mRNA, complete cds	
	101809	5.7	M86849	Homo sapiens connexin 26 (GJB2) mRNA, complete cds	
	133272	3.2	AA465016	ESTs; Highly similar to serine protease homolog	
	100365	4.8	D78811	mesoderm specific transcript (mouse) homolog	
	126818	4.7	AA305536	EST176522 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end, mRNA sequence.	
	132543	4.6	AA417152	ESTs; Highly similar to protein regulating cytokinesis 1 [H.sapiens]	
	103023	5.5	X53793	multifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase	
	132109	3.1	AA598801	ESTs	
	104037	3.5	AA372830	differentially expressed in hematopoietic lineages	
	104978	3.5	AA088458	ESTs; Weakly similar to [H] ALU SUBFAMILY J WARNING ENTRY [H] [H.sapiens]	
	108895	3.0	AA121316	ESTs	
	107248	3.8	D59894	ESTs	
	132902	3.4	AA480969	ESTs	
	120104	4.0	W95477	ESTs	
	128790	4.0	AA291725	secreted frizzled-related protein 4	
	101923	3.8	S75258	HNL=neurophil lipocalin [human, ovarian cancer cell line OOC6, mRNA Partial, 534 nt]	
	118943	3.4	W86835	copine III	
	130848	3.9	AA075427	ESTs	
	132358	3.5	X60488	H4 histone family; member G	
	106286	3.2	AA434441	frizzled (Drosophila) homolog 7	
	117567	2.3	N33920	diubiquitin	
	129691	3.3	X08700	collagen, type III; alpha 1 (Ehlers-Danlos syndrome type IV; autosomal dominant)	
	114767	4.5	AA148885	minichromosome maintenance deficient (S. cerevisiae) 4	
	100335	3.8	D63391	platelet-activating factor acetylhydrolase; isoform Ib; gamma subunit (29kD)	
	134989	3.5	AA236324	ESTs; Weakly similar to [H] ALU CLASS A WARNING ENTRY [H] [H.sapiens]	
	110009	3.4	H10933	ESTs	
	124059	4.0	F13673	ESTs	
	104755	2.2	AA024482	ESTs; Weakly similar to epidermal type I keratin [H.sapiens]	
	107151	3.4	AA821169	ESTs	
	132669	2.9	AA188378	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN L22 [H.sapiens]	
	104394	5.5	H46617	yp19h1.1 Soares breast 3NtHBst Homo sapiens cDNA clone IMAGE:187921 5' mRNA sequence	
	117697	2.5	N39214	ser-Thr protein kinase related to the myotonic dystrophy protein kinase	
	104954	3.3	AA074514	ESTs; Moderately similar to (define not available 4753768) [H.sapiens]	
	132994	3.7	AA505133	ESTs	
	102881	3.7	U72761	karyopherin (importin) beta 3	
	103988	2.2	AA314779	ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]	
	132183	2.5	L19183	Human MAC30 mRNA; 3' end	

FIGURE 13A

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118695	3.0	N71781	ESTs
100552	3.4	HG2167-HT22Protein Kinase H131, Camp-Dependent	
120471	2.5	AA251829	ESTs; Moderately similar to (define not available 4680697) [H.sapiens]
128547	4.2	U47732	transmembrane 4 superfamily member 3
108057	3.3	AA417067	ESTs
125103	4.0	T95333	ESTs; Weakly similar to Strabismus [D.melanogaster]
135243	3.4	AA215333	ESTs
121457	2.5	AA411448	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]
131216	2.7	D31058	ESTs
112971	2.4	T17105	ESTs
111178	2.1	N67239	ESTs
123533	2.3	AA808751	ESTs; Moderately similar to [!!!] ALU SUBFAMILY SC WARNING ENTRY [!!!] [H.sapiens]
105175	2.4	AA186804	ESTs; Weakly similar to unknown [S.cerevisiae]
105156	2.7	AA172372	ESTs; Moderately similar to [!!!] ALU SUBFAMILY SQ WARNING ENTRY [!!!] [H.sapiens]
111223	2.5	N68021	ESTs; Weakly similar to neogenin [H.sapiens]
132180	2.7	AA405569	fibroblast activation protein; alpha
106400	2.1	AA447821	ESTs
129260	3.1	AA093834	ESTs; Highly similar to (define not available 4678014) [H.sapiens]
115291	3.9	AA279843	ESTs
128628	2.1	C14037	ESTs; Weakly similar to Yel007c-ap [S.cerevisiae]
116399	2.7	AA599729	Homo sapiens homeobox protein A10 (HOXA10) gene; complete cds
130887	3.5	R45698	ESTs
105082	2.6	AA143763	ESTs; Weakly similar to Similarity to S. Pombe BEM1/BUD5 suppressor [C.elegans]
103453	3.2	X59585	H.sapiens mRNA for SMT3B protein
115947	2.6	AA443793	ESTs
105012	2.8	AA116036	ESTs; Highly similar to (define not available 4589929) [H.sapiens]
105507	3.2	AA256678	ESTs; Moderately similar to (define not available 4106061) [H.sapiens]
130800	2.6	AA223386	ESTs; Weakly similar to katanin p60 subunit [H.sapiens]
116451	3.4	AA621557	ESTs; Moderately similar to [!!!] ALU SUBFAMILY SQ WARNING ENTRY [!!!] [H.sapiens]
129945	2.5	AA232104	ESTs; Highly similar to (define not available 4929579) [H.sapiens]
100864	2.1	HG4297-HT45Transcriptional Coactivator Pct4	
128131	2.3	A1283182	claudin 3
131564	2.8	AA491465	ESTs
100279	3.1	D42084	Human mRNA for KIAA0094 gene; partial cds
134405	1.8	J04177	collagen; type XI; alpha 1
130287	2.6	AA113149	tumor suppressing subtransferable candidate 3
108828	2.1	AA131584	ESTs; Weakly similar to coded for by C. elegans cDNA cm1676 [C.elegans]
131289	2.2	AA485697	ESTs
109141	4.2	AA176428	ESTs
119307	2.5	T32108	ESTs
134319	2.1	AA129547	ESTs; Moderately similar to [!!!] ALU SUBFAMILY J WARNING ENTRY [!!!] [H.sapiens]
133458	5.0	M18728	non-specific cross reacting antigen
116732	2.3	F13779	ESTs; Weakly similar to [!!!] ALU SUBFAMILY J WARNING ENTRY [!!!] [H.sapiens]
116239	3.0	AA278850	ESTs

CGA8

## FIGURE 13B

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Code	PRIMEKEY	Size of tumor, ov	Accession	Complete title
CZA8	111929	3.7	R40057	prominin (mouse)-like 1
8CX2	128790	4.0	AA291725	secreted frizzled-related protein 4
CBC2	101809	5.7	M86849	Homo sapiens connexin 26 (GJB2) mRNA, complete cds
CBC1	100365	4.8	D78611	mesoderm specific transcript (mouse) homolog
CBC3	102618	2.5	U65932	extracellular matrix protein 1
CJA8	115697	8.1	AA411502	ESTs; Weakly similar to airway trypsin-like protease [H.sapiens]
CJA9	116176	5.7	AA463725	ESTs; Weakly similar to KIAA0226 [H.sapiens]
CGA7	115522	8.1	AA331393	ESTs
8CN5	112244	3.1	R51309	ESTs (now Sulfatase by in-house sequencing)
CQA1	132592	5.6	AA129390	ESTs
BCN7	117280	5.4	N22107	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]
CQA2	104660	6.0	AA007160	ESTs

## FIGURE 14

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## FIGURE 15

206 ACCATGATTACGCCAAGCTTGGCAGGAGACAGCCACTTGCCATGTCACCAAAACAAGGAGAAGGTGCAAGAC  
TGTCGGTGTGGACCTGACTCACAGCAGAAATCATTGAGAGATAAAATAAGTAA'FCCCACTGAATTCAGAAATCATGAAA  
AGCAGGAAAGCCAGGATCTCAGAGCTACTGCAAAAGTTCCCTTCTCCACCAGACGAGCACCAGAAAGCTGAGAATGCTGTT  
TCCTCAGGTAAACAGAGATTCAAAGGTACCTTCAGAAAGGAAAGAAATCTCTACACAGATGAGTCATCCAAACCTGGAAA  
AAATAAAAGAACTGCAATCACTACTCCAACTTTAAGAAGCTTCATGAAGCTCATTTTAAGGAAATGGAGTCCATTGATC  
AATATATTGAGAGAAAAAGAAACATTTGAAGAACACAATTCATGAATGAAGTGAAGCAGCAGCCCATCAATAAGGGA  
GGGGTCAGGACTCCAGTACCTCCAAGAGGAAGACTCTCTGTGGCTTCTACTCCCATCAGCCAACGACGCTCGCAAGGCCG  
GTCTTGTGGCCCTGCAAGTCAGAGTACCTTGGGTCTGAAGGGGTCCTCAAGCGCTCTGCTATCTCTGCAGCTAAACGG  
GTGTCAGGTTTTGAGCTGCTACTAAAGATAATGAGCATAAGCGTTCACTGACCAAGACTCCAGCCAGAAAGTCTGCACAT  
GTGACCGTGTCTGGGGGCACCCAAAAAGGCGAGGCTGTGCTTGGGACACACAAATTAAGACCATCACGGGGAATTCTGC  
TGCTGTTATTACCCCATTCAGTTGACAACAGGCAACGCAGACTCCAGTCTCCAATAAGAAACAGTGTGATCTTA  
AAGCAAGTTTGTCTCGTCCCTCAACTATGAACACACAAGGAAAGCTAAACCATGGGGCAATCTAAAGAAAATAAT  
TATCTAAATCAACATGTCAACAGAAATTAACCTCTACAAGAAAACCTACAACAACCCCATCTCCAGACAAAGGAAGACCA  
ACGGAAGAAACGCGAGCAAGAACGAAAGGAGAAAGCAAGGTTTGGGAATGCGAAGGGGCTCATTTTGGCTGAAG  
ATTAA

FIGURE 16

MTMITPSLARGQPLGHVTKTRRRCKTVRVDPDSQQNHSEIKISNPTEFQNHKEQESQDLRATAKVPSPPDEHQEAENAV  
SSGNRDSKVPSEGGKSLYTDESSKPGKNKRTAITPNFKKLHĖAHFKEMESIDQYIERKKKHFEHNSMNELKQQPINKG  
GV RTPVPPRGRLSVASTPISQRRSQGRSCGPASQSTLGLKGSLLKRSASAAKTGVRFSAAATKDNEHKRSLTKTPARKSAH  
VTVSGGTQKGEAVLGTHKLKTI TGN SAAVITPFKLTTEATQTPVSNKKPVFDLKASLSRPLNYPHKGKLPWGQSKENN  
YLNQHVNRINFYKKTYKQPHLQTKEEQRKKREQERKEKKAKVLGMRRGLILAED

## FIGURE 17

Amino-CKVLG MRRGL ILAED-COOH

**FIGURE 18**

Acetyl-KQPHL QTKEE QRKK-Amide

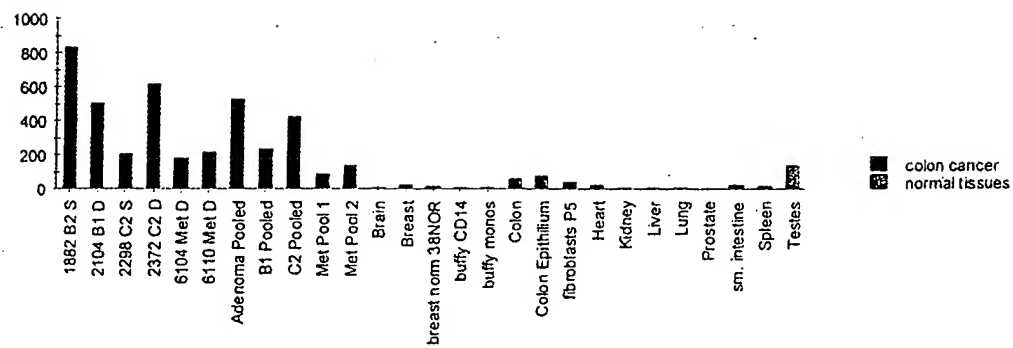
**FIGURE 19**

```

human_CAA2 -----KKHFEHNMSNELKQPINKGQVPTVPPGRLSVASTPISQRRS
mouse_CAA2 ARFKKMESIDEYEMRKKKKHLKEHSSLNELKLDKK--GIVTPVPEGRLSVPCTPARQQCP
          .....: : .....: :
human_CAA2 QGRSCGPASQSTLGLKGLKRSASAAKTGVRFSAATKDNEHKRSLTKTPARKSAHVTVS
mouse_CAA2 QG-----H--S-ATKMNVRFSAATKDNEHKCSLTKTPARKSPHVTAP
          ..          : : .....: :
human_CAA2 GGTQKGEAVLGTHKLKTITGNSAAVITPFKLTTATQTPVSNKKPVFDLKASLSRPLNYE
mouse_CAA2 GSASKGQAVFRTPKSKATERTSIAVITPFKLMTEATQTPSSSKKPVFDLKASLSRPLNYK
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
human_CAA2 PHKGKLPWQSKENNYLNQHVNRINFYKKTYPHLQTKKEQKKREQERKEKKAVLG
mouse_CAA2 PHKGKLPWQAKENNSLNERVSRVTFHRKTYKQPHLQTREERWKRQEERKEKKEKLE
          *****: : : : : : : : : : : : : : : : : : : : : : : :
human_CAA2 MRRGLILAED-
mouse_CAA2 ARRNLGVTKAQ
          **.* : :

```

# FIGURE 20

**FIGURE 21**

## FIGURE 22

GGTGGCCTCTGTGGCCGTCCAGGCTAGCGCGGCCCGCAGGCGCGGGGAGAAAGACTCTCTCACCTGGTCTTGCGGCTG  
TGGCCACCGCCCGCCAGGGGTGTGGAGGGCGTGTGCCGGAGACGTCCGCCGGGCTCTGCAGTTCCGCCGGGGGTGCGGC  
AGCTATGGAGCCGCGGCCACGGCGCCCTCTCCGGCGCCCGGGACTGGCCGGGGTGGGGAGACGCCGTGAGCCGCTG  
CGCTGGCCGCGAGCCAGGGTGGAACTGCCCGGCACGGCTGTGCCCTCGGTGCCGGAGGATGCTGCGCCCGGAGCCGGGAC  
GGCGCGGGGTCCCGATGAGGGCCCCGCGGGCGGGGACGGGCTGGGCAGACCCTTGGGGCCCCACCCGAGCCAGAG  
CCGTTTCCAGGTGGACCTGGTTTCCGAGAACCGCGGGCGGGCCGCTGCTGCGCGCGGGCGGGCGGGCGGCGAGCGCGG  
CGGCTGGTGTGGGGCGGGGCCAAGCAGACCCCCGCGGACGGGGAAGCCAGCGCGGAGAGCGAGCCAGCTAAAGGCAGC  
GAGGAAGCCAAGGGCCGCTTCCGCGTGAACCTTCGTGGACCCAGCTGCCCTCTCGTGGCTGAAGACAGCCTGTGAGATGC  
TGCCGGGGTGGAGTGCAGCGGCCCAACGTGAGCTTCCAGAACGGCGGGGACAGGTGCTGAGCGAGGGCAGCAGCCTGC  
ACTCCGGCGGGCGGGCGGGCAGTGGGCACCCAGCACTACTATTATGATACCCACACCAACCTACTACCTGCGCACC  
TTCGGCCACAACACCATGGACGCTGTGCCAGGATCGATCACTACCGGCACACAGCCGCGCAGCTGGGCGAGAAGCTGCT  
CCGGCCTAGCCTGGCGGAGCTCCACGACGAGCTGGAAAAGGAACCTTTTGAGGATGGCTTTGCAAAATGGGGAAGAAAGTA  
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CTCAATCTTAATGGTGAATCTTCTCTGTTGAAGTGAAGTTGTGAGAGTAGTTTTCTTGTACTTGAATAGCAATAAA  
AGCGTGTAACTTTTGG

# FIGURE 23

ATGGAGCCGCGGCCACGGCGCCCTCCTCCGGCGCCCCGGGACTGGCCGGGGTCCGGGAGACGCCGTGAGCCGCTGCGCT  
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 GCGGGGTCCGCGATGAGGGCCCCGCGGGCGGGACGGGCTGGGCAGACCCCTGGGGCCCCACCCGAGCCAGAGCCGT  
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 GGGTCTGGAGTCGACGGGCCAACGTCAGCTTCCAGAACGGCGGGGACAGGTCGTGAGCGAGGGCAGCAGCCTGCACTC  
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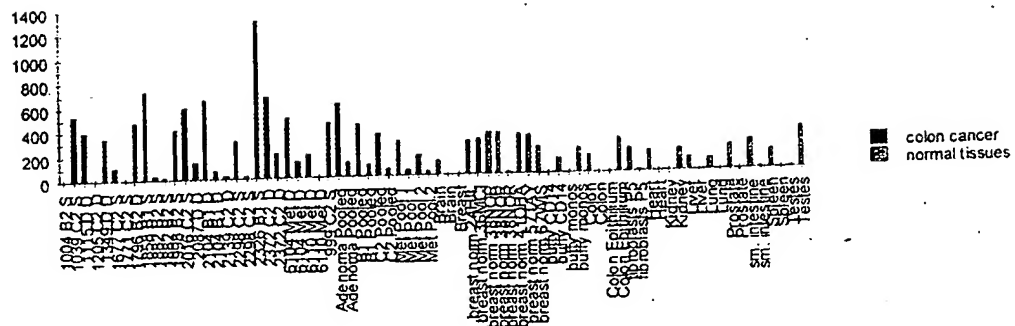
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YLLTTKKKWKDCKIRVFIGGKINRIDHRRAMATLLSKFRIDFSDIMVLGDINTKPKKENIIAFEEIIEPYRLHEDDKEQ  
DIADKMKEDEPWRITDNELEYKTKTYRQIRLNELLKEHSSTANIIVMSLPVARKGAVSSALYMAWLEALS KDLPPILLV  
RGNHQSVLTFYS

## FIGURE 24

## FIGURE 25

Peptide names	Solubility	
CAA9p1	1mg/1ml H2O	H-CDPAASSSSED\$LSLSD-NH2
CAA9p2	1mg/1ml H2O	Ac-KKSDLDT\$KPLSEKC-NH2
CAA9p3	1mg/1ml H2O	Ac-PLLKESKGPIVPLC-NH2
CAA9p4	min.amL DMSO/H2O	Ac-EHSILMIDEIC-NH2
CAA9p4MAPS	1mg/ml buffer pH7.5	Ac-EHSILMIDEIC-on 8-Branch Maps
CAA9p5	1mg/1ml H2O	Ac-DFREEETC-NH2
CAA9p5MAPS	1mg/1ml H2O	Ac-DFREEETC-on 8-Branch Maps

FIGURE 26



# FIGURE 27

GGCACGAGGAGAACTTAAAGAAATTCAGATATGTGAAGTTGATTTCCTGAAACCTCGTCA  
 TCCTCTGATGACAGTTGTGACAGCTTTGCTTCIGATAATTTTGCAAACACGAGGCTGCAGTCA  
 GTTCGGGAAGGCTGTAGGACCCGAGCCAGTGCAGGCACTCTGGACCTCTCAGGGTGGCGAT  
 GAAATTTCCAGCGCGGAGTACCAAGGGGAGCAACCAACAAAAAGCAGAGTCCCGCCAGCCCT  
 CAGAGAAATTCGTGACTGATTCCAACCTCGATTGAGAAGATGAAAGTGAATGAAATTTTTTGG  
 AGAAAAGGGCTTTAAATATAAAGCAAAACAAAGCAATGCTTGCAAACTCATGTCTGAATTA  
 GAAAGCTTCCCTGGCTCGTTCCGTGGAAGACATCCCTCCAGGCTCCGACTCAAAATCAAGG  
 AGACCGGAAGGCGTACATTCCCGGGTGTGCTTCCAGGAGAAACCTGAACGGAGAGCTCG  
 TCCTCTTACCAGGTCAAGGTCCCGGATCCTCGGGTCCCTTGACGCTCTACCCATGGAGGAGGA  
 GGAGGAAGAGGATAAGTACATGTTGGTGAGAAAGAGGAAGACCGTGGATGGCTACATGAAT  
 GAAGATGACCTGCCAGAACCCGTGCTNCAGATCATCCGTGACCTTCCGCATATAATTCCGC  
 CCAGTGGAAAGAAATACAGAAAGGAGAGGAGTTGGAGAACGTCTGCAGCAATCTCGAAGAGA  
 AGATTATAACCGTTCACTGGGYTCTACTTGTTCATCAATGCCGTGAGAAGACTATTGATACAA  
 AACAACTGCAGAAACCCAGACTGCTGGGGCGTTTCGAGGCCAGTTCTGTGGCCCTGCCTCG  
 AAACCGTTATGGTGAAAGAGGTGAGGATGCTGCTGGATCCGAACTGGCATTGCCCGCCTTG  
 TCGAGGAATCTGCAACTGCAGTTTCTGCCGCGAGCGAGATGGACGGTGTGCGACTGGGGTCT  
 TGTGTATTGCAAAATATCATGGCTTTGGGAATGTGCATGCCTACTTGAAAAGCCTGAAACA  
 GGAATTTGAAATGCAAGCATAATATCTGGAAAATTTGCTGCCTGCCTTCTACTTCTCAAATCTT  
 TCTTGTAAGGATTTCCAATTTTTTCACTGAAACCTGAGTTAAATCTTGATGATCAGCCTGT  
 TTCATAAGAACTCCAATCAAGTTAMTCTTAGCAGACATGTGTTTCTGGAGCATCACAGAAGG  
 TATATTGCTAGTTACACTTGGCCCTCCTGCAAGTTTCTCTGCTCCCAACCCCATCTCATAGC  
 ATTCCCTCTATTTTCCATTGGCTCCCTCTCCCAACCCGCTTAAGTTTCTGAATTTCTTTTA  
 AAWTTACAGTTTAAAGGAAAAGCCATATTTATTTACCTGGGTGTTGGAAATAGCCCTCCAT  
 AAAACCTTAAGCAGTTGGAACACAATAATAGTATTAACTAACTAGATCCTATTGAATTTCA  
 GAGAAGAGCCTTCTAACTTGTGTTACACAAAAACGAGTATGATTAGCATTCTACTAGTTGAA  
 ATTTTTAATAGAATCAAGGCACAAAAGTCTTAAACCATGTGGAAAAATTAGGTAATTTATKGC  
 ARATTGAKGGTCYCYCAATCCCAYGWATKSGCTTATGKTACMARKKGTGTGTCMAGTTTACG  
 ACYTAATTTTCYCTAATTTCTCYGSCCGAAGGKWAAGKGGKGGCTCCRGCTTACMCGATCAT  
 AATTTCMAAGGKTGGKGGSCAATGTAAVMCTTAATTAATAATKRWGGAAGAGCYATCTGG  
 AGATTAWGAGTAAGCTGATTGAAATTTTCAGTATAAACTTTAGTATAATTGTAGTTTGCAA  
 GKTTATTTAGTTTACATGTAAGGKATTGCMATAAATCTTTGGACAATTTTGKATGGAACT  
 TGATATTAAAACTAGTCTGTGGKCTTTGCAAGTTTCTTGTAAATTTATAAACCAGGCACAAG  
 GTTCAAGTTTAGATTTAAGCAGTTTATAACAATGATAAGTGCCTTTTGGAGATGTAACCTT  
 TAGCAGTTTGTAAACCTGACATCTCTGCCAGTCTAGTTTCTGGGCAGGTTTCTGTGTCAGTAT  
 TCCCTCTCTTTGCAATTAATCAAGGTATTTGGTAGAGGTGGAATCTAAGTGTGTTGATGTC  
 CAATTTACTTGCATATGTAAACCATGCTGTGCCATTCAATGTTTGTATGCATAATTGGAC  
 CTTGAATCGATAAGTGTAAATACAGCTTTTGTATCTGTAATGCTTTTATACAAAAGTTTATT  
 TTAATAATAAAATGTTTGTCTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA  
 CCCWTTAGTGAGKSWTAATTTAGCTTGGCACTGGCCGTCGTTTACAACGTCGTGACTGGGA  
 AAACCTGGCGTTACCAACTTAATCGCCTTGACGACATCCCTTTTCGCCAGCTGGCGTAA  
 TAGCGAAGAGGGCCGACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGG  
 ACGCGCCCTGTAGCGGCGCAATTAAGCGCGGCGGGTGTGGTGGTTACGCSAGCGTGACCGCTA  
 CACTTGCCAGCGCCCTAGCGCCGCTCCTTTCGCTTCTTCCCTCCTTCTCGCMCGTTTCGCCG  
 CTTTCCCAAGCTNTAAATCGGGC

One position equals 20 bases.  
■ if more than 2 bases disagree with consensus sequences  
/ if more than 10 positions are unknown  
- if more than 10 positions are gap characters

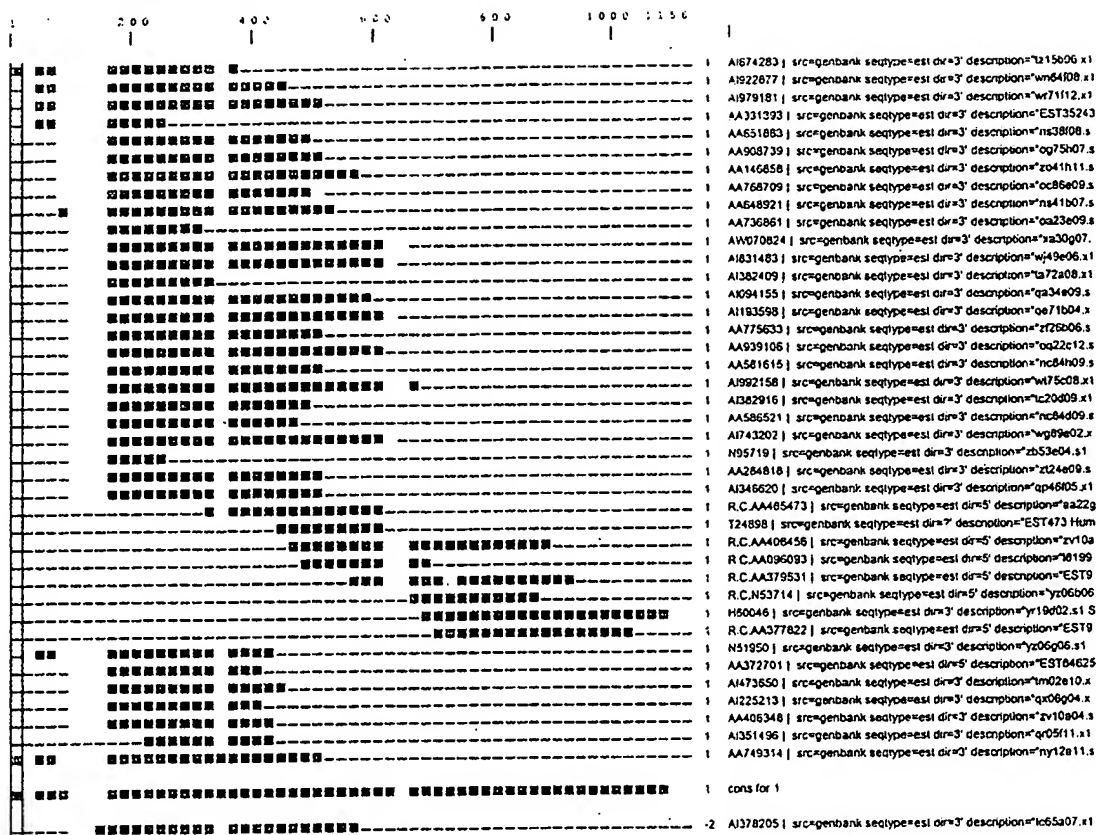


FIGURE 28A

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A1874283 | src=genbank seqtype=est dir=3 description="t215b06.x1 NCI\_CGAP\_U12 Homo sapiens cDNA clone IMAGE:2288527 3', mRNA s" src=gbcu7129773  
A1922677 | src=genbank seqtype=est dir=3 description="wn64108.x1 NCI\_CGAP\_Lu19 Homo sapiens cDNA clone IMAGE:2450247 3', mRNA s" src=gbest13651553  
A1979181 | src=genbank seqtype=est dir=3 description="wr71112.x1 NCI\_CGAP\_U11 Homo sapiens cDNA clone IMAGE:2493167 3', mRNA s" src=gbest13746306  
AA331393 | src=genbank seqtype=est dir=3 description="EST35243 Embryo, 8 week I Homo sapiens cDNA 3' end, mRNA sequence." src=gbest113/573  
AA651863 | src=genbank seqtype=est dir=3 description="ns38108.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1185927 3', mRNA s" src=gbest11753268  
AA908739 | src=genbank seqtype=est dir=3 description="og75h07.s1 NCI\_CGAP\_Ov8 Homo sapiens cDNA clone IMAGE:1454173 3', mRNA s" src=gbest10/20752  
AA146858 | src=genbank seqtype=est dir=3 description="z041h11.s1 Siratagene endothelial cell 937223 Homo sapiens cDNA clone IM" src=gbest10/20752  
AA769709 | src=genbank seqtype=est dir=3 description="oc86e09.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1356816 3', mRNA s" src=gbest19/36742  
AA648921 | src=genbank seqtype=est dir=3 description="ns41b07.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1186165 3', mRNA s" src=gbest11750927  
AA738661 | src=genbank seqtype=est dir=3 description="ca23e09.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1305832 3', mRNA s" src=gbest11870299  
AW070824 | src=genbank seqtype=est dir=3 description="xa30g07.x1 NCI\_CGAP\_Bu18 Homo sapiens cDNA clone IMAGE:2568348 3', mRNA s" src=gbest138/61005  
A1931483 | src=genbank seqtype=est dir=3 description="w45e06.x1 NCI\_CGAP\_Lu19 Homo sapiens cDNA clone IMAGE:2406178 3', mRNA s" src=gbest135/22416  
A1382409 | src=genbank seqtype=est dir=3 description="ta72a08.x1 Soares\_talal\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:20" src=gbest126/68899  
A1094155 | src=genbank seqtype=est dir=3 description="qa34e09.s1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:1688680 3', mR" src=gbest123/18508  
A1193598 | src=genbank seqtype=est dir=3 description="oe71b04.x1 Soares\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone IMAGE:17443" src=gbest124/35326  
AA775633 | src=genbank seqtype=est dir=3 description="z126b06.s1 Soares\_fetal\_heart\_Nb1H18W Homo sapiens cDNA clone IMAGE:3780" src=gbest19/43614  
AA591106 | src=genbank seqtype=est dir=3 description="oa22c12.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA clone IMAGE:1587094 3', mRNA s" src=gbest12/82353  
AA581615 | src=genbank seqtype=est dir=3 description="z126b06.s1 Soares\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone IMAGE:797537 3', mRNA se" src=gbest16/43395  
A1992158 | src=genbank seqtype=est dir=3 description="w175c08.x1 Soares\_thymus\_NHFTt Homo sapiens cDNA clone IMAGE:2513294 3'" src=gbest137/59215  
A1382916 | src=genbank seqtype=est dir=3 description="tc20d09.x1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:2064401 3', mR" src=gbest126/69408  
AA586521 | src=genbank seqtype=est dir=3 description="nc84d09.s1 NCI\_CGAP\_GC1 Homo sapiens cDNA clone IMAGE:797483 3', mRNA se" src=gbest16/48254  
A1743202 | src=genbank seqtype=est dir=3 description="wg99e02.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE:237" src=gbcu8/18434  
N95719 | src=genbank seqtype=est dir=3 description="zb53c04.s1 Soares\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone IMAGE:30732" src=gbest16/55806  
A2484818 | src=genbank seqtype=est dir=3 description="z124e09.s1 Soares\_ovary\_tumor\_NbHOT Homo sapiens cDNA clone IMAGE:714088" src=gbest12/8311  
A13446620 | src=genbank seqtype=est dir=3 description="qp46f05.x1 NCI\_CGAP\_Co8 Homo sapiens cDNA clone IMAGE:1926081 3', mRNA s" src=gbest126/33599  
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T24898 | src=genbank seqtype=est dir=5 description="EST473 Human colorectal cancer Homo sapiens cDNA clone 17B12, mRNA seque" src=gbest114/23757  
R.C.AA406456 | src=genbank seqtype=est dir=5 description="z10a04.r1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:753156 5', mRN" src=gbest114/23757  
R.C.AA096093 | src=genbank seqtype=est dir=5 description="18199.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5', " src=gbest19/36451  
R.C.AA379531 | src=genbank seqtype=est dir=5 description="EST92378 Skin tumor I Homo sapiens cDNA 5' end, mRNA sequence." src=gbest113/48697  
R.C.H53714 | src=genbank seqtype=est dir=5 description="yr19d02.s1 Soares\_fetal\_liver\_spleen\_1NFLS Homo sapiens cDNA clone IMAGE" src=gbest14/55137  
H60046 | src=genbank seqtype=est dir=3 description="z05g06.s1 Soares\_multiple\_sclerosi\_2NbHMSF Homo sapiens cDNA clone IMA" src=gbest15/12908  
R.C.AA377822 | src=genbank seqtype=est dir=5 description="EST30803 Synovial sarcoma Homo sapiens cDNA 5' end, mRNA sequence." src=gbest113/48698  
H51950 | src=genbank seqtype=est dir=3 description="tm02e10.x1 NCI\_CGAP\_Co14 Homo sapiens cDNA clone IMAGE:2155434 3', mRNA s" src=gbest128/8505  
AA372701 | src=genbank seqtype=est dir=5 description="EST84625 Colon adenocarcinoma IV Homo sapiens cDNA 5' end, mRNA sequence" src=gbest113/41867  
A1473650 | src=genbank seqtype=est dir=3 description="x05g04.x1 NCI\_CGAP\_Lym12 Homo sapiens cDNA clone IMAGE:2000598 3', mRNA s" src=gbest124/66524  
A125213 | src=genbank seqtype=est dir=3 description="zv10a04.s1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:753198 3', mRN" src=gbest114/23649  
AA406348 | src=genbank seqtype=est dir=3 description="q05f11.x1 Soares\_talal\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:19" src=gbest126/38475  
A1351496 | src=genbank seqtype=est dir=3 description="ny12a11.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1271516 3', mRNA s" src=gbest19/17507  
A1749314 | src=genbank seqtype=est dir=3 description="ny12a11.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1271516 3', mRNA s" src=gbest19/17507

cons for 1

A1378205 | src=genbank seqtype=est dir=3 description="tc65a07.x1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:2069480 3', mR" src=gbest126/64605

FIGURE 28B

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NETSSSSDD S CDSFASDNFA NTRLQSVREG CSTRSQCRHS GFLRVAMKFF  
ARSTRGATNK KAESRQPSN SVTDSNSDSE DESGMNFLEK RALNIKONKA  
MLAKLMSELE SFPGSFGRH PLPGSDSQSR RFRRTFPGV ASRRNFERRA  
RPLTRSRRI LGS LDALPME EEEEEDKYML VRKRKTVDGY MNEDDLPRTR  
RYRSSVTLPH IIRPVEEIQK ERSWRTSAAI LEEKIITVHW ALLVINAVRR  
LLIPKQTAET QTAGAFEASS VAPAFETVMV KRSGMLCWIR TGIARLVEES  
ATAVSAGSEM DGVRLGSLCI

## FIGURE 29

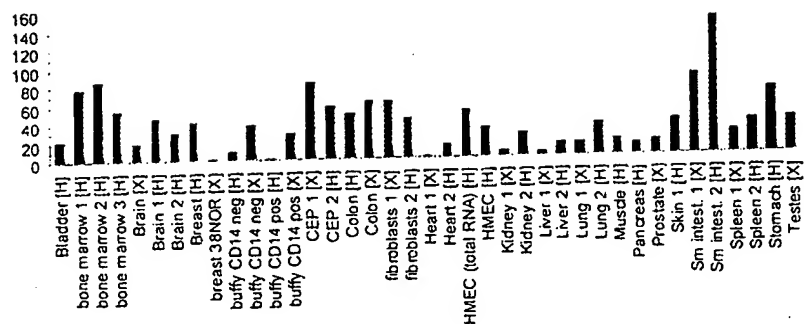


FIGURE 30A

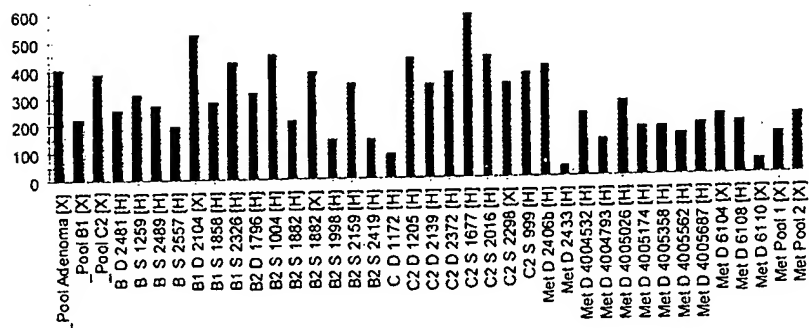


FIGURE 30B

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ACTCACTATNGGGCGAATGGGCCCTCTNNATGTCATGCTCGAGCGCCCGCCAGTGTGATGGATA  
TCTGCAGAATTTCGCCCTTAAGCAGTGGTAACAACGCAGAGTACGCGGGGGGAGACCGGAGGG  
CAGAAAGCAGAGTCCAGGCTTAGACTGCAGTTCCTCGCTTACCTGTGCAGTCTAATTTTGAGC  
TGCCTCTTTGTAGTCTTAAAAGGCAGGAGCTTCGTGTTGTGGGTCTGCTAACCCGTACGTTTC  
GTGGGCAAGTCGTGTGTACTCCTCGCCCTGCTCAGCTCCAAACACGCTTCTACACTGATAAC  
AAGAAATATGCCGTAGATGATGTTCCCTTCTCAATCCCTGCTGCCTCTGAAATTGCCGACCTTA  
GTAACATCATCAATAAACTACTAAAGGACAAAAATGAGTTCCACAAACATGTGGAGTTTGATT  
TCCTTATTAAGGGCCAGTTTCTGCGAATGCCCTTGACAAACACATGGAAATGGAGAACATCT  
CATCAGAAAGAAGTTGTGGAAATAGAATACGTGGAGAAATATACTGCACCCAGCCAGAGCAA  
TGCAATGTTCCATGATGACTGGATCAGTTCAATTAAAGGGGCAGAGGAATGGATCTTGACTGGT  
TCTTATGATAAGACTTCTCGGATCTGGTCCTTGGAAAGGAAAGTCAATAATGACAAATTGTGGGA  
CATACGGATGTTGTAAGATGTGGCCTGGGTGAAAAAAGATAGTTTGTCTGCTTATTATTG  
AGTGCTTCTATGGATCAGACTATTCTTATGGGAGTGGAAATGTAGAGAGAAAAAAGTGAA  
AGCCCTACACTGCTGTAGAGGTCTGCTGGAAGTGTAGATTCTATAGCTGTTGATGGCTCAGG  
AACTAAATTTTGCAGTGGCTCCTGGGATAAGATGCTAAAGATCTGGTCTACAGTCCCTACAGA  
TGAAGAAGATGAAATGGAGGAGTCCACAAATCGACCAAGAAAGAAACAGAAAGACAGAACAG  
TTGGGACTAACAGGACTCCCATAGTGACCTCTCTGGCCACATGGAGGCAGTTTCCTCAGTT  
CTGTGGTCAGATGCTGAAGAAATCTGCAGTGCATCTTGGGACCATACAAATTAGAGTGTGGGT  
GTTGAGTCTGGCAGTCTTAAGTCAACTTTGACAGGAAATAAAGTGTTAATTGTATTTCCTATT  
CTCCACTTTGTAAACGTTTAGCATCTGGAAGCACAGATAGGCATATCAGACTGTGGGATCCCC  
GAACTAAAGATGGTTCCTTGGTGTGCTGTCCTAACGTCACATACTGGTTGGGTGACATCAG  
TAAATGGTCTCCTACCCATGAACAGCAGCTGATTCAGGATCTTTAGATAACATTGTTAAGC  
TGTGGGATACAAGAAAGTTGTAAGGCTCCTCTCTATGATCTGGCTGCTCATGAAGACAAAGTTC  
TGAGTGTAGACTGGACAGACACAGGGCTACTTCTGAGTGGAGGAGCAGACAATAAATTGTAT  
TCCTACAGATATTCACCTACCACTTCCCATGTTGGGGCACTAAGTGAAACAATAATTTGACTA  
TAGAGATTATTTCTGTAATGAAATTGGTAGAGAACCATGAAATTACATAGATGCAGATGCA  
GAAAGCAGCCTTTTGAAGTTTATATAATGTTTTCACCTTCATAACAGCTAACGTATCATT  
TTCTTATTTTGTATTTATAATAAGATAGGTTGTGTTTATAAAATACAACTGTGGCATACA  
TTCTCTATACAACTTGAAATTAACCTGAGTTTACATTTCTCTTTAAARGTAAAAA  
AAAAA

## FIGURE 31

One position equals 17 bases.

- if more than 1 bases disagree with consensus sequences.
- if more than 6 positions are unknown.
- if more than 6 positions are gap characters.

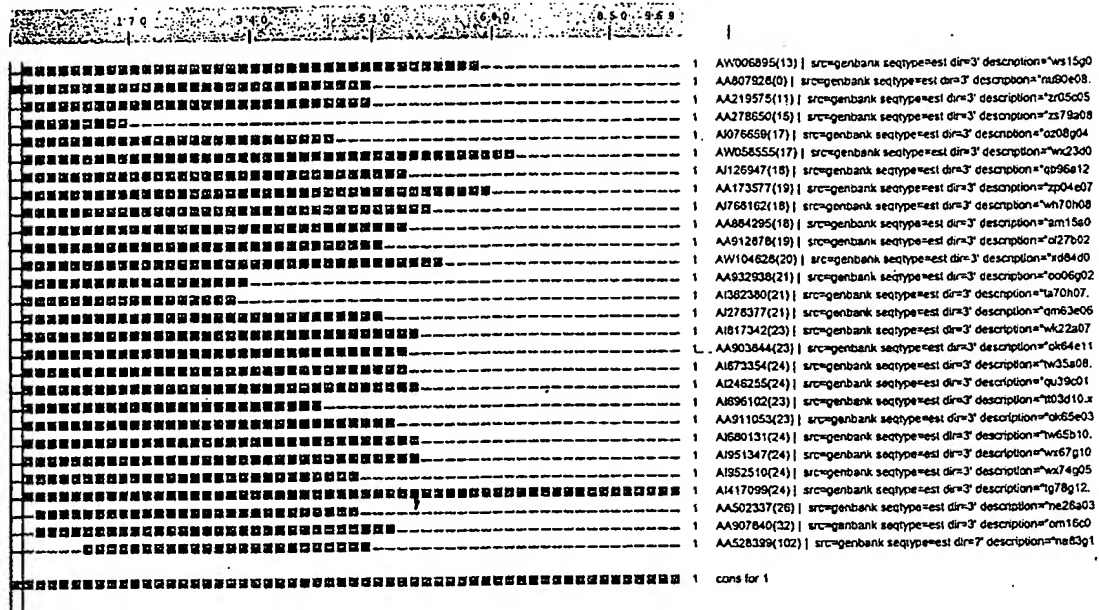


FIGURE 32A

AW006895(13) | src=genbank seqtype=est dir=3 description="w15g01.x1 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:2497296 3' siml" src=gbest3776306  
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AA219575(11) | src=genbank seqtype=est dir=3 description="zr05c05.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA c" src=gbest11122843  
AA278650(15) | src=genbank seqtype=est dir=3 description="zr78a08.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:703670 3', mRNA s" src=gbest124143  
A076659(17) | src=genbank seqtype=est dir=3 description="wz23d07.x1 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:2544493 3' siml" src=gbest3851329  
A105855(17) | src=genbank seqtype=est dir=3 description="wz08g04.x1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IM" src=gbest234960  
A1126947(18) | src=genbank seqtype=est dir=3 description="zr04e07.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone I" src=gbest3350375  
AA173577(19) | src=genbank seqtype=est dir=3 description="wz04e07.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone I" src=gbest3350375  
A1766182(18) | src=genbank seqtype=est dir=3 description="wz04e07.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone I" src=gbest3350375  
AA084295(16) | src=genbank seqtype=est dir=3 description="am15a06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1468866 3' " src=gbest2065489  
AA912878(19) | src=genbank seqtype=est dir=3 description="o27b02.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1524651 3' " src=gbest216292  
A104628(20) | src=genbank seqtype=est dir=3 description="o27b02.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1524651 3' " src=gbest216292  
AA932938(21) | src=genbank seqtype=est dir=3 description="o27b02.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1524651 3' " src=gbest216292  
A032360(21) | src=genbank seqtype=est dir=3 description="ta70h07.x1 Soares\_fetal\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:20" src=gbest2668381  
A0278377(21) | src=genbank seqtype=est dir=3 description="qm63e06.x1 Soares\_placenta\_8to9weeks\_2NbHP8to9W Homo sapiens cDNA clone " src=gbest2538348  
A0817342(23) | src=genbank seqtype=est dir=3 description="wz22a07.x1 NCI\_CGAP\_Lym12 Homo sapiens cDNA clone IMAGE:2413044 3' siml" src=gbest124143  
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A0673354(24) | src=genbank seqtype=est dir=3 description="wz39e01.x1 NCI\_CGAP\_U11 Homo sapiens cDNA clone IMAGE:2261654 3' similar" src=gbest317780  
A0246255(24) | src=genbank seqtype=est dir=3 description="qu39e01.x1 NCI\_CGAP\_U11 Homo sapiens cDNA clone IMAGE:2261654 3' similar" src=gbest317780  
A0696102(23) | src=genbank seqtype=est dir=3 description="t103d10.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2238699 3', mRNA s" src=gbest3130525  
AA911053(23) | src=genbank seqtype=est dir=3 description="o65e03.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA clone IMAGE:1518844 3' similar" src=gbest217487  
A060131(24) | src=genbank seqtype=est dir=3 description="wz65b10.x1 NCI\_CGAP\_U13 Homo sapiens cDNA clone IMAGE:2284539 3' similar" src=gbest3174554  
A0951347(24) | src=genbank seqtype=est dir=3 description="wz67g10.x1 NCI\_CGAP\_Br18 Homo sapiens cDNA clone IMAGE:2548770 3' siml" src=gbest37720164  
A0952510(24) | src=genbank seqtype=est dir=3 description="wz74g05.x1 NCI\_CGAP\_Ov38 Homo sapiens cDNA clone IMAGE:2549432 3', mRNA " src=gbest37721327  
A0417099(24) | src=genbank seqtype=est dir=3 description="tq78g12.x1 Soares\_NHMPu\_S1 Homo sapiens cDNA clone IMAGE:2114950 3' siml" src=gbest2733775  
AA502337(26) | src=genbank seqtype=est dir=3 description="wz26a03.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:898444 3', mRNA se" src=gbest1548530  
AA907840(32) | src=genbank seqtype=est dir=3 description="om15c08.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1541198 3' " src=gbest214257  
AA528399(102) | src=genbank seqtype=est dir=7 description="he63g12.s1 NCI\_CGAP\_Ew1 Homo sapiens cDNA clone IMAGE:910918, mRNA seque" src=gbest1574499

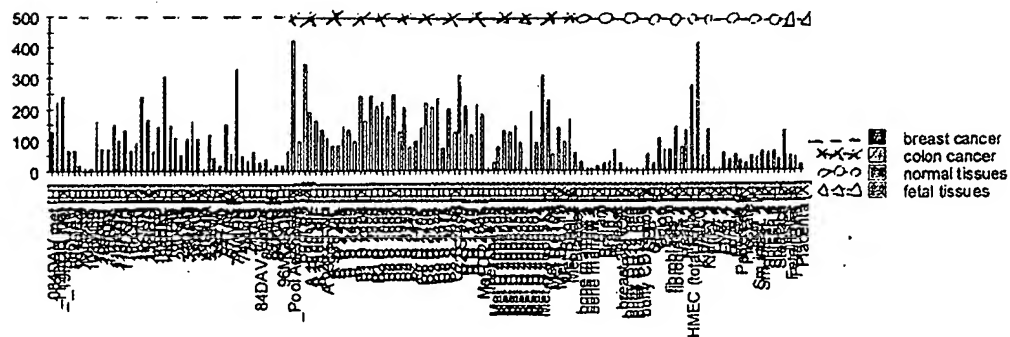
cons for 1

## FIGURE 32B

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MAQLQTRFYTDNKKYAVDDVPFSIPAASEIADLSNIINKLLKDKNEFHKHVEFDF  
 LIKGQFLRMPLDKHMEMENISSEEVVEIEYVEKYTAPQPEQCMFHDDWISSIKGA  
 EEWILTGSYDKTSRIWSLEGKSMITIVGHTDVVKDVAWVKKDSLSCLLLSASMD  
 QTILLWEWNVERNKV KALHCCRGHAGSVDSIAVDGSGTKFCSGSWDKMLKIWS  
 TVPTDEEDEMEESTNRPRKKQKTEQLGLTRTPIVTLSGHMEA VSSVLWSDAEEIC  
 SASWDHTIRVWVVESGSLKSTLTGNKVFNCISYSPLCKRLASGSTDRHRLWDPR  
 TKDGSLSLSLTSHGTGWVTSVKWSPTHEQQLISGSLDNIVKLWDTRSCKAPLYDL  
 AAHEDKVLSDWTDGTLSSGGADNKLYSYRYSPTTSHVGA.

# FIGURE 33



# FIGURE 34

### FIGURE 35

## FIGURE 36

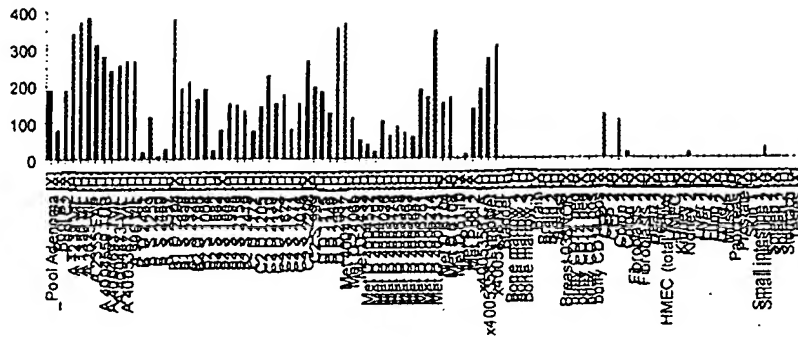


Figure 37

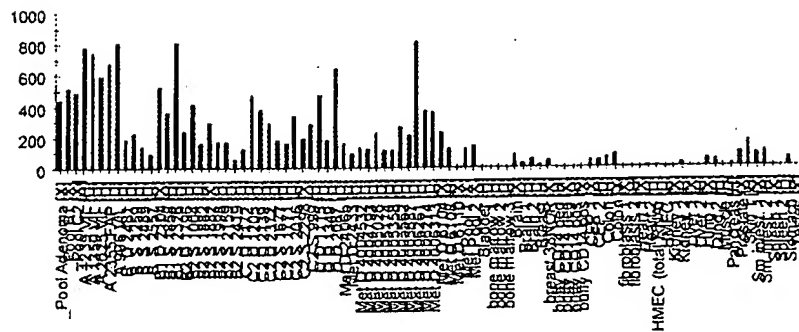


Figure 38

AGAATCCCTCGGCTCCITTCGCCGCCGGTATTCTGSGTATATGATCCCACTCTCACTCTCATAGGAGAC  
GATCTCGAAGTAGATCATATACACCAGAAATACCGCCCGGGAAGGAGCCGAAGCTCAAGGGTAAAGACAGTA  
GAAATATTATTAGTAACAATAATGTGTGAACCTTTAAGATGGATAATAGGCGATGGACTGAGTGCTGCT  
ATCTTGAAATGTGCACAGGTACACTTACCTTTTTTTTTTTTTTTTAAAGTTTTCCCATTCAGGATAACA  
ACATTGTGATCTGTACTACAGGAACCAATGTTCATGCGTCATACATGTGGCTATAAAGTACAT/AAATATA  
TCTA/CTATTTCAT/ATGTGGGGTGGGTAATCTGTCTGTGAAAT/AA/GTAA/AGCTTTTCACTTAAAAA  
AATGCATTACTTTCACTTAACTAGACACCCAGGTCGAAATTTTCAAGGTTATAGTACTTATTTCAACAA  
TTCTTAGAGATGCTAGCTAGTGTGAAGCTAAAAATAGCTTTATTTATGCTGAATTGTGATTTTTTATGC  
CAAAATTTTTTAGTTCTAATCATTGATGATAGCTTGGAAATAAATAATTATGCCATGGCATTGACAGTT  
CATTTATTCCTATAAGAA/TAAATTGAGTTTAGASAGAAATGGTGGTGTGAGCTGATTATTACAGTTACTG  
AAATCAATATTTATTTGCTACATTATTCATTGTATTTAGGTTTCCTTTTACATTCTTTTATATGCA  
TTCTGACATTACATATTTTAAAGACTATGGAPAT/ATTTAA/AGATTTAAGCTCTGGTGGATGATTATCTG  
CTAAGTAAGTCTGAAATGTAAATCTTGTAAATACTGTAATATACCTGTACAC/AAATGCTTTTCTAATG  
TTTTAACCTTGAGTATTCCAGTTGCTGCTTTGTACAGAGGTTACTGCAATAAAGGAAGTGGATTCAAT/AA  
CCTAAAAA/AAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 39

CCAAGTCTACCTCATGTTGGAGGATCTTGCTAGCTATGGCCCTCGTACTCGGCTCCCTGTTGCTGCTGG  
 GGCTGTGCGGGMCTCCTTTTCAGGAGGGGAGCCCTTCATCCACAGATGCTCCTAAGGCTTGGAAATTATGAA  
 TTGCTGTGCAACAAATTATGAGACCCAGACTCCCATAAAGCTGGACCCATTGGCATTCTCTTTGAACTAGT  
 GCATATCTTTCTCTATGTGGTACAGCCGCGTGATTTCAGAGAGATACTTTGAGAAATTCTTACAGAAAGG  
 CATATGAAATCCAAATTTGATTATGACAAAGCCAGAACTGTAACTTTAGGTCTAAAGATTGTCTACTATGAA  
 GCAGGGATTATTCTATGCTGTGTCCTGGGGCTGCTGTTTATTATTCTGATGCCTCTGTTGGGGTATTCTT  
 TTGATATGTGCTGTTGCTGTAACAAATGTGGTGGAGAAATGCACCAGCGACAGAAAGAAATGGGGCCCTCC  
 TGAGGAAATGCTTTGCAATCTCCCTGTTGGTGATTGTATATAATAAGCATTGGCATCTTCTATGGTTTT  
 GTGGCAATCACCAGGTAAGAACCCGATCAAAAGGAGTCGGAACTGGCAGATAGCAATTTCAAGGACTT  
 GCGAACTCTCTTGAATGAATCCAGAGCAATCAAAATATATTTGGCCAGTACAACACTACCAAGGACA  
 AGGCGTTCCACAGATCTGAACAGTATCAATTCAGTCTAGGAGCGGAATTTCTGACCGACTGAGACCCCAAC  
 ATCATCCCTGTTCTTGAATGAGATTAACTCCATGGCAACAGCGATCAAGGAGACCAAGAGGGCGTTGGAGAA  
 CATGAACAGCACCTTGAAGAGCTTGCAACAAAGTACACAGCTTAGCAGCAGTCTGACCAAGCTGAAAL  
 CTAGCCTCCGGTCTCTCAATGACCCCTCTGTGCTTGGTGCATCCATCAAGTAACTGCAACAGCATC  
 AGATTGTCTCTAAGCCAGCTGAATAGCAACCCCTGAATGAGGAGCTTCCACCCGTTGGATGCAGAACTGA  
 CAACTGTAATAAGCTTCTTAGGACAGATTGGATGGCTTGGTCCAAACAGGGCTATCAATCCCTTAATGATA  
 TACCTGACAGAGTACAAACCCAAACCAAGCTGTGCTAGCAGGTATCAAAAGGGCTTGAATTCATTTGGT  
 TGAGATATCGCAATGTAACTCAGCGCTTCTCTATTAGGATATACTCTCAGCATTCTCTGTTTATGTAA  
 TAACTGAAAGTTACATCCACAGAAATTTACCTACATTGGAAGATGATTCAATCTGTTGGCTGGGTG  
 GGCTGATGACAGGCTGCAACCCCGAGCCAGGCTGTGCTCCAAACCCGAGGCGCTCTCTCTCATGGT  
 TGGAGTTGGATTAAGTTTCTCTTTTGTGGATATGATGATCATTGTGGTTCTTACCTTTGTCTTTGGTG  
 CAAATGTGGAAAACTGATCTGTGAACCTTACACGAGCAAGGAATTATTCGGGTTTGGGATACCCCTAC  
 TTAATTAATGAAGCTGGGAATATCTCTCTGGAAGCTATTTAATAAATCAAAATGAAGCTCACATT  
 TGAACAAAGTTACAGTGACTGCAAAAAAATAGAGGCACTTACGGCACTCTTACCTGCAGAACAGCTTCA  
 ATATCAGTGAACATCTCAACATTAATGAGCATACITGGAAGCATAAGCAGTGAATTGGAAAGCTGAAAGTA  
 AATCTTAATATCTTTCTGTTGGGTGCAGCAGGAAGAAACCTTCAGGATTTTGCTGCTTGTGGAAATAGA  
 CAGAAATGAATATGACAGTACTTGGCTCAGACTGGTAAATCCCCCGCAGGAGTGAATCTTTATCATTG  
 CATATGATCTAGAAGCAAAAGCAAAACAGTTTGGCCCAAGAAATTTGAGGAACTCCCTGAAAGAGATGCA  
 CAAACTATTAAACAAATTCACAGCAACGAGTCTTCTCTATAGAACAATCACTGAGCACTCTATACCAAG  
 CGTCAAGATACTTCAACGCAACAGGGAATGGATTGTTGGAGAGATTAAGTATAGCTTCTCTGGAAT  
 TTGCTCAGAACTTCATCACAACAAATCTCTCTGTTATTATTTAGGAAACTAAGAGATGGAAGAAACA  
 ATAAATAGGATATTTTGAACATTTCTGCACTGGATCGACTTCTCTATCAGTGAGAAAGTGGCATCGTGCA  
 ACCTGTGGCCACCGCTCTAGATACTGCTGTTGATGCTTTCTGTGTAGCTACATTATCGACCCCTTGAAT  
 TGTTTTGGTTTGGCATAGGAAAGCTACTGATTTTACTTCCGGCTCTAATTTTGGCGTAAACTGGCT  
 AAGTACTATCGTGAATGGATTGGAAGGACGTGTACGATGATGTTGAAACTATACCCATGAAAAATATGGA  
 AATGGTAAATATGGTTATCAAAAGATCATGTATATGGTATTCACAACTCTGTTATGACAGCCCATCAC  
 AACATTGATAGCTGATGTTGAAACTGCTTGAGCATCAGGATACCTAAAGTGGAAAGGATCACAGATTTTGG  
 GTAGTTTCTGGGTCTACAAGGACTTTCACAAATCCAGGAGCAACGCCAGTGGCAACGTAGTGACTCAGGCGG  
 GCACCAAGGCAACCGCACCATTTGGTCTCTGGGTAGTGCTTTAAGAAATGAACACAATCACGTTATAGTCCAT  
 GGTCCATCACTATTCAAGGATGACTCCCTCCCTTCTGCTATTTTGTTTTACTTTTACACTGAGT  
 TTCTATTTAGACACTACAACATATGGGGTGTTTGTTCCATTGGATGCATTCTATCAAACTCTATCAA  
 TGTGATGGCTAGATTCTAACATATTGCCATGTGTGGAGTGTGCTGAACACACACCACTTTACAGGAAAGAT  
 GCATTTTGTGTACAGTAAACGGTGTATATACCTTTTGTACCAAGAGTTTAAACAAATGAGTATTAAT  
 AGGACTTTCTTAAATGAGCTAAATAAGTCACCATTTGACTTCTTGGTGTGTTGAAATTAATCCATTTTC  
 ACTAAAGTGTGTGAACCTACAGCATATTCTTACGCAAGAGATTTCTATCTATTAATCTTTATCAAGAT  
 TGGCCATGTTCCACTTGGAAATGGCATGCAAAAGCCATCATAGAGAACTGCGTAACCTCTGACAA  
 TTCAAAGAGAGAGACAGATCTTGAGAGAGAAATGCTGTTCCGTTCAAAGTGGAGTTGTTTAAACAGATGC  
 CAATTACGGTGTACAGTTTAAACAGAGTTTCTGTTGCATTAGGATAAACATTAATTTGGAGTGCAGCTAACA  
 TGAGTATCATCAGACTAGTATCAAGTGTCTAAATGAATATGAGAGATCCTGTGCACAACTCTTAGATC  
 TGGTGTCCAGCATGGATGAAACCTTTGAGTTGGTCCCTAAATTTGCATGAAAGCACAAGGTAATTTCA  
 TTTGCTTCAGGAGTTTCTGTTGGATCTGTCAATTAACAAAGTATCAGCAATGAAGAACTGGTCCGACAA  
 AATTTAACCTTGATGTAATGGAATCCAGATGTAGGCATTCCCCCAGGCTTTTCTATGTGCAGATTGCA  
 TTCTGATTCAATTTGAATAAAAGGAACCTTG

FIGURE 40

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CAGCGGCGGCTGAATTCTAGGGCGGGTTCGGCGCCCGAAGGCTGAGAGCTGGCGCTGCTCGTGGCCCTGTG  
TGGCAGACGGCGGAGCTCCGCGGCCGACCCCGCGGCCCGCTTTGCTGCCGAC:GGAGTTTGGGGGAAG  
AAACTCTCTCTGCGCCCCAGAAAGATTCTTCTCGGCGAAGGGACAGCGAAAGATGAGGGTGGCAGGAAGA  
GAAGGCGCTTTCTGTCTGCGGGGGTGGCAGCGCGAGAGGGCAGTGCCATGTTCTCTCTCCATCCTAGTGGC  
GCTGTGCTGTGGCTGCACCTGGCGCTGGCGGTGGCGGGCGGCCCTGCGAGGCGGTGGCATCCCTATG  
TGCCGGCACATGCCCTGGAACATCACGCGGATGCCAACCACCTGCACCACAGCAGCAGGAGAACGCCA  
TCCTGGCCATCGAGCAGTACGAGGAGCTGGTGGACGTGAAGTGCAGCGCCGTGCTGGCTTCTTCTCTG  
TGCCATGTACGCGCCCATTTGCACCCCTGGAGTTCCTGCACGACCCCTATCAGCCGTGCAAGTCCGTGTGC  
CAACGCGCGCGGCGGAGCTGGCAGCCCTCATGAAGATGTACAACCAAGCTGGCCCGAAAGCTTGGCCT  
GCGACGAGCTGCTGTCTATGACCGTGGCGTGTGCATTTGCGCTGAAGCCATCGTCACGGACCTCCCGGA  
GGATGTTAAGTGGATAGACATCACACCAGACATGATGTTACAGGAAGGCCCTCTTGATGTTGACTGTAAA  
CGCCTAAGCCCCGATCGGTGCAAGTGTAAAAGGTGAAGCCACCTTGGCAACGTATCTCAGCAAAACT  
ACAGCTATGTTATTCAATGCCAAATATAAGCTGTGCAAGAGGAGTGGCTGCAATGAGGTCAACGGTGGT  
GGATGTAAAAGAGATCTTCAAGTCTCATACCCATCCCTCGAAGTCAAGTCCCGCTCATTACAAATCT  
TCTTGGCAGTGTCCACACATCCTGCCCATCAAGATGTTCTCATCATGTGTTACGAGTGGCGTTCAAGGA  
TGATGCTTCTTGAATTTGCTTAGTTGAAAAATGGAGAGATCAGCTTAGTAAAAGATCCATACAGTGGGA  
AGAGAGGCTGCAGGAACAGCGGAGAACAGTTCAGGACAGAAAGAAACAGCCGGCGCACCAGTCTGAT  
AATCCCCCAAACCAAGGGMAAGCCCTCCTGCTCCCAACAGCCAGTCCCAAGAGAAACATTAAACTA  
GGAGTGGCCAGAGAGAACAAACCCGAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAGACTTCCGAC  
TTCCTTACAGGATGAGGCTGGGCATTGCTGGACAGCTTATGTAAGGCCATGTGCCCTTGGCCCTAACCA  
ACTCACTGCAGTGTCTTATAGACACATCTTGCAGCATTTTCTTAAAGCTATGCTTCAGTTTCTCTT  
CTAAGCCATCACAAGCCATAGTGGTAGGTTTGGCCCTTGGTACAGAGGTGAGTTAAAGCTGGTGGAAA  
GGCTTATTTGCATTGCATTGAGATAACCTGTGTGCATCTCTAGAGAGTAGGGAATAATGCTTGTTA  
CAATTCGACCTAATATGTGCATTGTAAATATAATGCCATTTTCAAAACAAACAGTAATTTTTCACAG  
TGTGTTTTATACCTTTTGATATCTGTGTTGCAATGTTAGTGTATTTTTAAATGTGATGAAATATAA  
TTTTTGTGATGAAAGGGGATTTTTGAAAAATTAGAGAAGTAGCATATGGAAATATAATGTGTTTTT  
TACCAATGACTTCAGTTTCTGTTTTAGCTAGAACTTAAAAACAATAATAATAAAGAAAAATATA  
AAAAAGGAGAGGCGAGACATGTCTGGATTCTGTTTTTTGGTTACCTGATTCCATGATCATGATGCTTC  
TTGTCAACACCCCTCTAAGCAGCACCAGAACAGTGAGTTTGTCTGTACCATTAGGAGTtaggTACTAAT  
TAGTTGGCTAATGCTCAAGTATTTTATACCCACAGAGGATGTCACTCATCTTACTTCCAGGACAT  
CCACCCCTGAGAAATAATTTGACAGCTTAAATGGCCTTCATGTGAGTGCACAAATTTGTTTCTCTCAT  
TTAAATATTTTCTTTGCTTAAATACATGTGAGAGGAGTTAAATATAATGTACAGAGAGGAAAGTTGAGT  
TCCACCTCTGAATGAGAATTACTTGACAGTTGGGATACTTTAATCAGAAAAAGAACTTATTTGCAGC  
ATTTTATCAACAAATTTCTAATTTGTGGACAAATGGAGGCATTATTTTAAAAACAATTTTATGGCCT  
TTTGCTAACACAGTAAGCATGTATTTTATAAGGCATTCAATAAATGCACACGCCCAAGGAAATAAAT  
CCTATCTAATCTACTCTCCACTACAGAGGTAATCACTATTAGTATTTGGCATATTATCTCCAGGT  
GTTTGTCTATGCACCTATAAATGATTTGAACAAATAAACTAGGAACCTGTATACATGTGTTTCATAAC  
CTGCCTCCTTTGCTTGGCCCTTTATGAGATAAGTTTTCCTGTCAAGAAAGCAGAAACCATCTCATTCT  
AACAGCTGTGTTATATCCATAGTATGCATTACTCAACAACTGTGTGCTATTGGATCTTAGGTGGT  
TCTTCACTGACAACTAGTAATAACATCTCACCGGAATTC

FIGURE 41

GAATTAATCCTATGACAACTAAGTTGGTTCGTCTCACCTGTTTGGTCAGGTTGTGTAAGAGTTGGT  
GTTTGCTCAGGAAGAGATTTAAGCATGCTTGCTTACCCAGACTCAGAGAAGTCTCCCTGTTCTGTCTTAG  
CTAIGTTCTGTGTTGTGTGTCATTCTGTTTCCAGAGCAAACCGCCAGAGTAGAAGTTGATTGGGGC  
ACGCTGCAGACGATCCTGGGGGTTGTGAACAACTCCACCAGCATTGGAAAGATCTGGCTCACCGTCC  
TCTTCATTTTCCGATTAATGATCCTCGTTGTGGCTGCAAGGAGGTGTGGGGAGATGAGCAGGCCGACTT  
TGTCTGCAACACCCCTGCAGCTGATCTTCGTGTCCAGCCCAGCGCTCCTAGTGGCCATGCACGTGGCCATCC  
CGGCTATGGGCCCTGCAGCTGATCTTCGTGTCCAGCCCAGCGCTCCTAGTGGCCATGCACGTGGCCATCC  
GGAGACATGAGAGAAGAGGAAGTTCATCAAGGGGGAGATAAAGAGTGAATTTAAGGACATCGAGGAGAT  
CAAAACCCAGAAAGTCCGCATCGAAGGCTCCCTGTGGTGGACCTACACAAGCAGCATCTTCTCCGGGT  
ATCTTCGAAGCCCGCTTCAATGTACGTTCTCTATGTCTGTACGACGGCTTCTCCATGCAGCGGTGGTGA  
AGTGCACCGCTGGCCCTTGTCCCAACACTGTGGACGCTTGTGTCTCCGGGCCACGGAGAAGACTGTCTT  
CACAGTGTTCATGATTGCAGTGTCTGGAATTTGCATCCTGCTGAATGTCACTGAATGTGTTATTGCTA  
ATTAGATATTGTTCTGGGAAGTCAAAAGCCAGTTTACCGCATTGCCAGTTGTTAGATTAGAAATAG  
ACAGCATGAGAGGGATGAGGCAACCCGTGCTCAGCTGTCAAGGCTCAGTCGCCAGCATTTCCCAACACM  
AGATTCTGACCTTAAATGCAACCATTTGAAACCCCTGTAGGGCTCAGGTGAAACTCCAGATGCCCAATG  
AGCTCTGCTCCCTAAAGCCTCAAAACAAAGGCTTAATCTATGCCTGTCTTAATTTCTTTCACTTAAG  
TTAGTTCCACTGAGACCCAGGCTTTAGGGGTTATTGGTGAAGGTAATTTCAATTTTAAACAGAGGA  
TATCGGCNTTTGTTCTTTCTCTGAGGCAAGAGAAAAAGCCAGGTTCCACAGAGGACACAGAGAAGGT  
TTGGGTGTCCTCCTGGGGTTCTTTTGCCAACTTTCCCCACGTTAAAGGTGAACATTGGTTCTTTCAATTT  
GCTTTGGAAATTTTAACTCTTAACAGTGGACAAAGTTACAGTGCCCTTAAACTCTGTTACACTTTTGGGA  
AGTGAAAACTTTGTAGTATGATAGGTTATTTTGATGTAAGATGTTCTGGATACCATTATATGTTCCCCC  
TGTTTCAGAGGCTCAGATTGTAAATGTAATGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTATG  
GTCCTTTGGTTATGAATACTTTGCAGCACAGCTGAGAGAGGCTGTCTGTTGTTATTCATTGTGGTCTATAGC  
ACCTAACCAACATTGTAGCCTCAATCGAGTGAGACAGACTAGAAGTTCCTAGTTGGCTTATGATAGCAAAAT  
GGCCTCATGTCAAATATTAGATGTAATTTGTGTAAGAAATACAGACTGGATGTACCACCACTACTACC  
TGTAATGACAGGCTGTCCAAACATCTCCCTTTCCATGCTGTGGTAGCCAGCATCGGAAGAACGCTG  
ATTTAAAGAGGTGAGCTTGGGAATTTTATTGACACAGTACCATTAAATGGGGAGACAAATGGGGGCA  
GGGGAGGGAGAGTTTCTGTCTTAAACAGGTTTGGAAAGACTGGACTCTAAATTTCTGTTGATTAAAG  
ATGACCTTTGCTACCTTCAAAAGTTTGTGTTGGCTTACCCCTTCAGCCTCCAATTTTAAAGTGAAT  
ATAACTAATAACATGTGAAAGAATAGAGCTAAGGTTTAGATAAATATTGAGCAGATCTATAGGAAGAT  
TGAACCTGAATATTGCCATTATGCTTGACATGGTTTCCAAAAATGGTACTCCACATCTTCAGTGAGGG  
TAAATATTTTCTGTTGTCAAGAATAGCATTTGTAAGCATTTTGTAAATAAAGAAATAGCTTTAATGA  
TATGCTTGTAACATAAATAATTTGTAATGTATCAATACATTTAAAAATTAATAATCTCTATAA  
T

FIGURE 42

CGGCCAGCACACCCCGGCACCTCCTCTGCGGCAGCTGCGCCTCGCAAGCGCAGTGGCCGACGGCACGCCG  
GAGTGGCTGTAGCTGCCCTCGGCGCGGGCTGCCGCCCTGCGGGCTGTGGGGCTGCGGGCTGCGCCCCCGCT  
GCTGGCCAGCTCTGCACGGCTGCGGGCTCTGCGGCGCCCGTGTCTGCAACGCTGCGGCGGGCGGCATG  
GCATACGCGGCCCATGGTGGCGCGAGATCGCCTCCGAGGATGAGGGAGTGGTGGGTCCAGGTGGGGCTG  
CTGGCCGTGCCCTGCTTGTGCGTACCTGCACATCCACCCCTCAGCTCTCCCTGCCCTTCACTCAT  
GCAAGTCTTCAGGCAAGTTTTCACTTACAAGGGACTGCGTATCTTCTACCAAGACTCTGTGGGTGTGGT  
TGGAGTCCAGAGATAGTTGTGCTTTTACACGGTTTCCAACATCCAGCTACGACTGGTACAAAGATTGG  
AAGGGCTCTGACCTTGAGGTTTCATCGGGTGATTGCCCTTGATTCTTAGGCTTTGGCTTCAGTGACAAAC  
CGAGACCACATCACTATTCCATATTTGAGCAGGCCAGCATCGTGGAGCGCTTTGCGGCATCTGGGGCT  
CCAGAACCGCAGAAATCAACCTTCCTTCTCATGACTATGGAGATATTGTTGCTCAGGAGCTTCTCTACAGG  
TACAAGCAGAAATCGATCTGGTGGCATAACCAAGAGTCTCTGTCTGTCAATGGAGGTATCTTTCCCTG  
AGACTCACCGTCCACTCCTTCTCCAAAGCTACTCAAGATGGAGGTGTGCTGTCAACCATCTCTACACG  
ACTGATGAACCTCTTTGTATTCTCTGAGGTCTCACCCAGTCTTTGGGGCGTATCTCGGCCCTCTGAG  
ACTGAGCTGTGGGACATGTGGGCGAGGATCCGCAACAATGACGGGAACTTAGTCATTGACAGTCTCTTAC  
AGTACATCAATCAGAGGAAGAAGTTCAAGAGCGCTGGGTGGGAGCTCTTGCTCTGTAACATATCCCAT  
TCATTTTATCTATGGGCCATTGGATCCTGTAAATCCCTATCCAGAGTTTTGGAGCTGTACAGGAAACG  
CTGCCGCGGTCCACAGTGTGATTTCTGGATGACCACATTAGCCACTATCCACAGTAGAGGATCCCATGG  
GCTTCTTGAATGCATATATGGGCTTCATCAACTCCTTCTGAGCTGGAAAGAGTAGCTTCCCTGTATTACC  
TCCCTACTCCCTTATGTGTTGTGATTCCACTTAGGAACAAATGCCAAAGAGGTCTTGGCCATCAAA  
CATTAATCTCTACAAAGTCCACTTTACTCAATTTGGTGAACAGTGTATAGGAAGAAGCCAGCAGGAGCT  
CTGACTAAGGTTGACATAATAGTCCACCTCCCATTACTTTGATATCTGATCAATGTATAGACTTGGCTT  
TGT'TTTTGTGCTATTAGGAAATCTGATGAGCACTACTATTCACTGATGCAGAAAGAGCTTCTTTTGCA  
TAAAGACTTTTTTAACTTTGGACTTCTCTGAAATATTTAGAAGTGCTAATTTCTGGCCACCCCC  
AACAGGAATCTATAGTAAGGAGGAGGAGAAGGGGGCTCCTTCCCTCTCCTCGAATGACGTTATGGGCA  
CATGCCTTTTAAAGTTCTTTAAGCAACACAGAGCTGAGTCCCTTTGTCATACCTTTGGATTAGTGT  
TCATCAGCTGTTTTAGTTATTAACATTTGTTAAATAGATATTGGTTTAAATGATACAGTATTTAGG  
TATGATTTAAGACTATGATTTACCTATACATTATATATTTTATAAGATACTAAACCAGCATACCTT  
ACTCTGCCAGAGTAGTGAAGCTAATTAACACGT'TTGGTTTCTGAATAAATTGAACATAATCCAACTAT  
TTCCTAATAACACAGGACATTAAGGACCAATAGCATCTGTGCCAGAGATGTACTGTATTAGCTGGGAAG  
ACCAATTCTAACAGCAATTAACAGTCTGAGACTCCTCATACCTCAGTGGTTAGAAGCATGTCTCTCTTGA  
CCTACAGTAGAGGGGAAGGGATTGTTGTGTAGTCAAGTCAACCTGCTGAATGTACACTGATTCCTTTATG  
ATGACTGCTTAAC'TCCCCACTGCC'TGTCCCAGAGAGGCTTCCAATGTAGCTCAGTAATTCCTGTACTT  
TACAGACAGGAAAGTTCCAGAACTTTAAGAACAACCTCTGAAGACCTATGAGCAATGGTGTCTGAATA  
CTTT'TTTTAAAGCCACATTTATTGTCTTAGTCAAGCAGGATTATTAAGTGATTATTTAAATTCGT  
TTTTTAAATTAGCAACTTCAAGTATAACAACCTTGAATCTGGAATAAGTGTTATTTTCTATTATAAA  
AATGAATTTGTGACAAAATAAACC

## FIGURE 43

CTCTGAGTGTCCAGTGGTCAGTTGCCCGAGGATGGGACCACAGCCAGAGCAGCCTTGGTCTTGACCTAT  
TTGGGCTGTGCTTCTGCTGCCTCTGAGGGAGGCTTCACGGCTACAGGACAGAGGCAGCTGAGGCCAGAGC  
ACTTTCAGAGAGTTGGCTACGCAGCTCCCCCTCCCCACCCCTATCCCGAAGCCTCCCCATGGATCACCC  
TGACTCCTCTCAGCATGGCCCTCCCTTTGAGGGACAGAGTCAAGTGACGCCCTCCCTCTCAGGAGGCC  
ACCCCTCTCCAAACAGGAAAGCTGCTACCTGCCCACTCCCTGCTGAAAGGAAGTGGGTCCCCCTCTCC  
CTCAGGAAGCTGTCCCCCTCCAAAAGAGCTGCCCTCTCTCCAGCACCCCAATGAACAGAAGGAAGGAAC  
GCCAGCTCCATTGGGGACCACAGCCATCCAGAACCTGAGTCTTGGATGCAGCCACAGCACTGCCAACAG  
GACCGGTCCCAAGGGGGCTGGGGCCACCGGCTGGATGGCTTCCCCCTGGGGCGGCTTCTCCAGACAATC  
TGAACCAATCTGCCCTTCTAACCCTCAGCATGTGGTATATGGTCCCTGGAACTACACAGTCCAGCTA  
CTCCACCTCACTCGCCAGGGTGAGACCTCAATTTCTGGAGATTGGATATTCCTGCTGCTGCCACTGC  
CGCACCCACACAAACCGCCTAGAGTGTGCCAACTTGTGTGGGAGGAAGCAATGAGCCGATTCTGTGAGG  
CCGAGTTCTCGGTCAAGACCCGACCCCACTGGTGTGCACGCGGAGGGGGAGGCTCGGTCTCTCTGCTT  
CCAGGAGGAAGCTCCCCAGCCACACTACCAAGCTCCGGGCTGCCAGCCATCAGCCTGATATTTCTCTG  
GGTCTTGAGCTCCCTTCTCTCTGGGGTGCCCACTTGGACAATATCAAGAACATCTGCCACCTGAGGC  
CCTTCCGCTCTGTGCCACGCAACCTGCCAGCTACTGACCCCTACAAAGGGAGCTGCTGGCACTGATCCA  
GCTGGAGAGGGAGTTCCAGCGCTGCTGCCCGCAGGGGACAACTCAACCTGTACATGGAAGGCCCTGGGAG  
GATACCCCTTGACAAATACGTGTACCGGGAGTATGCTGTGAAGACCCACCACTTGTGTGGCCGCCACC  
CTCCCAGCCCTACTCGGGATGAGTGCTTTGCCCGTCGGGCTCCTTACCCCACTATGACCGGGACATCTT  
GACCATTGACATCAGTCGAGTCACCCCAACCTCATGGGCCACCTCTGTGGAAACCAAGAGTTCTCACC  
AAGCATAAACATATTCCTGGGCTGATCCACACATGACTGCCCGCTGCTGTGACCTGCCATTTCCAGAAC  
AGGCTTGTGTGCAGAGGAGGAGAAATTAACCTTCATCAATGATCTGTGTGGTCCCCGACGTAACATCTG  
GCCAGACCTGCCCTCTGTGTACCTGAGTCTGGGGATGAACAGGTCAACTGCTTCAACATCAATTA  
CTGAGGACAGTGGCTCTAGTGTCTGGAGACACTGAGAACGCCAAGGGCCAGGGGAGCAGGGCTCAACTG  
GAGGAACAAATATCAGCTCCACCTCTGAGCCCAAGGAAGAAATGCTCACCCACAGGCCCTAGAGGGTCAG  
ATG

## FIGURE 44

**FIGURE 45A**

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CAAGATGGCTAGAAATGGTGGCTTTCTGAGTGTCTAAACTTGACACCCCTGGTAAATCTTTCACACACTT  
CCACTGCCCTGCCTAATGAAGTTTGGATTCAATTTTAACCACTGGAAATTTTCAATGCCGTCAATTTTCAGTT  
AGATGATTTTGCACCTTTGAGATTAAATGCCATGTCTATTGATTAGTCTTATTTTTTATTTTTACAGGC  
TTATCAGTCTCACTGTTGGCTGTCTATTTGTGACAAAGTCAATAAAACCCCAAGGACGACACACAGTATGGA  
TCACATATTGTTTGACATTAAAGCTTTTSCCAGAAATGTTGCAATGTGTTTACCTCGACTTGCTAAATCG  
ATTAGCAGAAAGCATGGCTAATAATGTTGTTGGTGAATAAAATAAATAAGTAAACAAWRAARAWNGC  
CTGCTCTCTCTGTGCTAGCCTCAAAGCGTTCATCATACATCATACCTTTAAGATTGCTATATTTGGGTT  
ATTTTCTTGACAGGAGAAAAAGATCTAAAGATCTTTTATTTTCATCTTTTGGTTTTCTTGGCATGACTA  
AGAAGCTTAAATGTTGATAAATATGACTAGTTTTGAATTTACACCAAGAACTTCTCAATAAAGAAATC  
ATGAATGCTCCAGATTTCAACATACCAACAGAGAAATTAATTTCTAACATTGTGTTCTATGATTATTTG  
TAAGACCTTCACCAAGTTCTGATCTTTTAAAGACATAGTTCAAAATTGCTTTTGAAATCTGTATTTCTT  
GAAAAATATCCTTGTGTATTAAGTTTTTAAATACCAGCTAAAGGATTACCTCACAGAGTATCAGTACC  
CTCCTATTACAGCTCCCCAAGATGATGTGTTTTGCTTACCTTAAGAGAGGTTTTCTTCTATTTTATGATA  
ATTCAAGTGTCTAGATAAATTATGTTTTCTTAAAGTGTATGTTAAACTCTTTAAAGAAAATTTAATAT  
GTTATAGCTGAATCTTTTGGTAACTTTAAATCTTTATCATAGACTCTGTACATATGTTCAAAATAGCTGC  
TTGCCCTGATGTGTATCATCGGTGGGATGACAGAACAAACATATTATGATCATGAATAATGTGCTTTGT  
AAAAAGATTTCAGTTATTAGGAAGCATACTCTGTTTTTAAATCATGTATAATATCCATGATACTTTTAT  
AGAACAATCTGGCTTCAGGAAAGCTAGAAGCAATATTTCTTCAAATAAAGGTGTTTAACTTTAAAAA  
AAAAAAAAAAAAAAAAAAAA

**FIGURE 45B**

CAAGAAATTCGGCAGGAGGGCGTGTCCAGAAAGTGTGGATACGTGTCAGTAGTTAATTCAGCTGGCAGGT  
TCCCTGAGTGCAGCTGGCTCGATAGTCGTAAATGAAGAGTGTGCCGAAAAGACTTTGAATCCAGTATGAA  
TGTAGTACAGGAATTAATTTAAGTCTAGGATCAGAGGGACTGAAGACTGGGCTCCTCCTAGATTTCAAA  
TCATATTTAATATTCATCCACCACTCAAGAGGGACCTTGTGGTGGCAGCCAGAAATTTTCTGTGCCGGC  
TGTGGAACTCCAGTAGAGCCTAAGTTTGTGAGCGGCTCCGGTACTGCGAATACCTAGGGAAGTATTTCTG  
TGACTGCTGCCACTCATATGCAGAGTCGTGCATCCCTGCCGGAATCCTGATGATGTGGGACTTCAAGAAGT  
ACTACGTCAGCAATTTCTCCAAACAGCTGCTCGACAGCATATGGCACCAGCCATTTTCAATTTGCTGAGC  
ATCGGGCCAAAGCCTGTATGCGAAAGCCAAAGGAGCTGGACAGAGTGAAGGAAATTCAGGAGCAGCTCTTCCA  
TATCAAGAAGCTGTGGAAGACCTGTAGGTTTGTATACAGTGCATTAAGGGAGTTCCAGCAGGTCGCGGA  
CACTTGACTGATGACTCCACCTGTCTCTCCCTTAGGACCTGGTCAGGATCAAGAAAGGGCTGCTGGCACCTT  
TACTCAAGGACATTTCTGAAAGCTTCCCTTGCACATGTGGTGGCTGTGAGCTGTGTCAAGGAAAGGGCTTT  
ATTTGTGAATTTTCCAGAATACGACTGTCTATCTTCCATTTCAGACAGCAACATGTAGAAAGTGTTCAGC  
GTGCAAGGGCTTGTCTTCAAAACAGTGTCTCCAGTCCCTCCGAGTGCCCCGGTGTGCGAGGATCACAGCGA  
GGAGAAACTTCTGGAAAGTGTGGCTCTGCAAGCAACATGTGCCCCCTGAGTACTGTGAAAAAGACTGTTC  
AACATGCCCTTATGATAACACCGATTTGTGTCTATTATTGGTGACATTTGTTTAGATATTGGGTATTGTATA  
TTAAGGAAAAAGATGGTCTATATTCTCTTTATTCATATACTTAATGTTTCAAGAAATGCAGATTCTGTG  
TTAAGCACAGGGCTGATAGTTGTGGTTTGTCTTACAAATGTTCTGTTTGGCTGCTATTGGTTTTTAA  
GAGGTTTTTTATACTTTTGTATTGTAATAGTTATGTTTCACTGATGCTGAGCCAGTTTGTATGTGTGTGCA  
TATATGTGAAGTGAAGTGAAGATGAATTAAGTCAAGTTTCTCTTTCTCTAAAGCTTGTGTGATGAACTG  
GTTGGTCTTTCAAGTGMAMAAAWATATGACCCCAAAAAAAAAAAAAAAAAAAGCAATGCGAAGGTG  
CTAATCCTGACGCTCGTGGTGGCCGCTGCGGCTTCTGCTGAGCAGCAATGGGCGACAAAGGAAGAA  
CAGGGCCCTGCCCCACCGTTGCTGGACGCCGAACCCGCG

## FIGURE 46

GGAAATTTATAGATCTTGATATTGAATCCATCAGTGATTCAAGAGATACACCTATTTGCCTAAAACAACCTA  
ACATGTATTGGTTATGGAATCATGTGTTGGATAGGTTCTTAAGACCTGTTCCTCAAATCTTGACACAGTT  
TTCAAGGGTGGCTTATTGACTTGCCAGGTTGGGAGATAATCCAGATTACCTAAGATTGGGTAAAAAGT  
CATCTGTGACTTTGCTGCGAGGGCATTTCCTAAGTGGAGTACAGGATCTAAAGGGTTTTCTTAGAAAGGG  
CAATATTTGCTCAATGAAGTAAGCAGAAGGACTCTGGGTTAGAAGCATCTGCACAAAACTGGTGAGACCTA  
CTCTCCACTGCTCTGCAGCTGGATGGCTGATGGCAGGCTGAGCAGTGGGGAAGCAGGTTTTAACAACAGGG  
AGTCTTTCCAGGTCAGTGTATTTGAGAAAGAAACATAAACTATTTGCTGTTACATTCCGAGGTGAGCCTT  
CTTCTTTACGTTTTATAATATGCAATGCCAGCTTCTGGAAGCAAGTATCATCATGTACCAATGCTTTA  
TACACCATCACATTCATGAATTTTTCAGTGGTCAGAACTTGTGTAATATGTCTCTTAGATGATTTTGG  
GGAGATGTGATTTATTTTTCATATTTTCAAAATGCATTTTCAATTAAGTTATCTATTGAGACAAAC  
GAAAAAAAAAAAAAAAAAAAAA

## FIGURE 47

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AATTTTGGGCCCTCGMAGGCCG/AGAAATTCGCGCCACCGANGGAATTTTGGTACCACCCAGGGG  
 GAAATGGAATGCTCTTTCAAACCTTAGTTCCTTCCTTCTCTGATGCTGGCCTTTGACACAAAT  
 CTGGTAGAAGAAGCCTATGAATTTAGGGGCACTGTGACCTCCCTGCGCCCAAGAGTTCTTGGAGAG  
 AAGTAGCAAGAAATTTGGAACACGGCGGTGGAGGGCGSGTGGATGGCCATGGGCTGGGCCCTCCGTATCAGCG  
 CTGCTCACCTTSCCTGGGAGCTTATTCCTGATCTCATTTGAATGTTCCAGAGGGAGCATCATMAGAGCCCA  
 GAGCTCCGATTTCCAAAGATGTATTTGACATTTATGGAGATTTGCTGTATCATATTTTGATAAAATCT  
 AACCTATTTTGTTGGSGTTTGGTTGTCTTGTCTTAGGACCTGGTAGTTTATTTGGTGTATTTTTTCTC  
 CGTTATTTTCTACATAGGCCAAGAGAAATTCGAGGGATGACACAGCTCCCAAGAAAAGTGAAGTGGTGGGAGA  
 GAAATTTGCTTTTTTCTTTTCTTTCTTTCTTAGTTTTCTTGGCTGAGATTTCCGTGCAAGACGACAC  
 CCAATAGCTATTAGAGTTGACATTTGACATTTAAATGGGCGCATGGCTCATTTGTAGATAGTAGAAGG  
 TGCTCTCCCTTGTCTCAAGCTCATATGACAGAGCTGCTGACAGCTGGGAGTCTGTGGCCCTCTCTACGCG  
 AGAGGGCTTTAAGCTGGACACAGACGCGCTAGGCTGGGCGAGGATGGGACCCATGGCCCCCTCTTAGA  
 GSAACGGCTCTCGGTTAGSAAAGGACAGCTGGGGGTGCTGCTATAATAGTTACGTGTCACCGTGCTTT  
 TATGAGTAGGTGTTTTGTGCACTTGCCAGGGGTTTTCTCTCTGTGTGCGAGGGGAGTGATTAAAGCAATGS  
 TGCTCGAGTAGAGCTTACAAATTTAATAGACTTTTCTTATCATATGCTCCATTTCTTCCCTGAAATAA  
 AATATACACAAAGCAAAAATAATGATAGTTTACATCTTATAGTTCCCTGCCCAACAAAGAAATTTCT  
 TAGTTCCACTGGCCAGGATTTTCTCATATGTGACAGCTTACACATTACTAGAGGCACACCCACCMAGGAG  
 TATTTGTGTCTACTTTATCTGTGACCCAGGCCACAAATACCCACATTTGGAAAGACCCATTTGTGATGGTAA  
 ACATCCCTCTCTGTCTCCACACACCTGTGACTGCCCTGCATGTGTTCTATGACCTCCGAAAGGCCCTAAT  
 CATGAAGCAGCAAAACCAGCAGATCTCCACCCCTGCTCAGGACCTCTGCTGAAGAGGGGATGAAGTG  
 GGTCTCCAGGGAGGACATGGGGGCTTTGTGGGAGCTGGCTCGGAGAGCCGGCTTACAGGAGGGACAGCTGT  
 CAGTTGGGAGGGGACCGCTCCGAGGAGGACAGGCGCTACACACCCCACTCTACTTATCATCCCTGCT  
 CACACACCTTTGTCCAAGGCTTTATGCAATCGAATTTATTTTCCAATCGAGAGGACAGTGATAGATGCAT  
 TTTTCCAGGCTGTCTCAGAAAGGCTCGCTAAATGTATGACTTTGTGCAGAAATGCTGAGATCTCCCCCACT  
 TTTGGTTTGTGACAGTAAAAACTCTTCCACTGTGACTTATTTTCTCTCGAGGAGCCAGGACCTGTG  
 TCCCTTGTGCTGACTTAGCACAGTGGCCAGGATCCAATACGAGTCCAGGGGTGACCGCAGGATGGTGGGG  
 GCAGCGGGCTCTCCACTACCCGACCCAGGAGCCCTGACGCACTGCTCCCTGCACTCTCAGCAGCATCC  
 CTGTGCACAGCTGGAGGGTGATGCGCCGCTCACTTTGTTGATGAGTGGGTGAAACGCTGATGATACAG  
 CTCTTCCCTGCCGTGCCCTGCCACGGAGCAGGCATTGTGAACGTGGCTGGTGTGTCAGTCCACAGTGGCA  
 TGGCTTCCGCGCCACACCAACAGTGGAGAGCTGGAGACAGGGCAATGAGTCTGTGTCGGGCGAGCTGGACATC  
 CCCCATAGAGGGCCCCACAGCACTTAACAGGCAAGGCTCTGGGCATTCGCCGAGGAGGACTCAATGCTAA  
 ACCAAGCCTGCCCTGGCTCTGTGCCAGGGGCCCTCTCTGATTTTACACATCCATTTTACACAGACCCCTTC  
 CTCTTTATAAAGGCTGACAGTCTGTGTCGACCAAGAAACCCACAGCATGAAGACAGGAGTGAAGGGCC  
 TTTGTGCCCACTCCAGACACCTGCTGTGGGTTGTGACAGGCATGTTCTGTCTGTGCGCTGGTGG  
 TCTCGTGAGACAGTTCCGAGGACGGGGAATTTGACGGGTGGTGGGGCGTAGGCTTATATGTGGAACATG  
 TCGAGATCTCGCCTGACAGCGGATCTGGATATACATATGATATTTGACGTGTAATTTAAATATATATC  
 TGTTTGCCATCTGATAGAAAGATTATGTGAAGGCTCTGAGGAGAGGGAGATGACATTTCTGCCAGG  
 TCTTGGGACCTTATCCGAGTCAATGAAATTTGATGACTGTTGATCCAGTGGTGCAGAAAGCTACACTCCATG  
 TGTCACTACGCTTATGACTCTAATGATTTTAAAGGCAAAAATGACAGCGCATCCATCTTACCCCTC  
 GATTTCTCGATCCAGCTTTCTGTGCCAGTGTCTACTGAGCAACAGCTCTCGCCATCGGACCCCGG  
 TGGGCTCGAGTCTCGGGGACAGTTGCCATGGAGCCCTCTGGGTCTATTCTACAAATGTGCTGAGTGCCA  
 CTGAAACCCCAAGAGATGGAGTACCTTGGGCAAGCTTAAGAGAGAAGATTTCTCAGGGTATTTATA  
 GTGTGTCAGGAGGTCAGGAAGCAGGATGGAAGATGCATTCAGACTGTTAATTTATTAACAGGCAAA?  
 GATTTTGTGTTTCTTGATGACAGCTATTAAAGTTTGGGACTTATTTTCCCATTTGAGAGATTAATATATA  
 ATTTAAGATGATAGATTTCTGCTTAAGTTGTGCTCTTCAAGCTTCAATGATTTAAGGAGCACTAAGGGTA  
 ATGATACCAATAGGGTTGGTTTATTATCAAACCTGAATAGCTGTGGTTTCTCCAGTAAATTTTCTTCT  
 ACTGAACATGGAGCCATTATTAAGAGTGTGTGTTTTTATTATGTACATTGTATATTTTGTGCTGT  
 TGAATGCTTATTTTCTTAATAGTTTCTTTTAGTTTCTTTAAAGTTGTGATAGTACTAGATTAGATTCTGATG  
 TAACTGCAATCAGTTGGTCTCTGCTGGGCTCTCTCTGTTTATTACTTTAAGGACAGTGTAGTTG  
 TCGTCCACCACCTTTCAAAAAATGTGPAACTGCCCTGCCCTCCCTTTTGTCTGACAACTGTGTACATTG  
 ACCACTTCTTACCATCTATTATGTTGAAATCAAACTCTTTTGGTGACATTCTCATGCTCTGTGCAAA  
 TCTGAATATACTCATGGCTTCCAAATAAAAAAABAAAAA

### FIGURE 48

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genome IE-35

490 JAB016492.1 Homo sapiens hJTB gene, complete cds e-I 18

491 X98176 H.sapiens mRNA for MACH-beta- I protein IE-36

Homo sapiens **huntingtin interacting protein**

HYPK mRNA,

492 AF049613 partial cds 7E-22

493 AF039690.1, HomosapiensantigenNY-CO-8 (NY-CO-8)mRNA, partial cds IE-37

INM-001003I Homo sapiens ribosomal protein, large, PI ribosomal

494 phosphoprotein PI mRNA, complete cds. 4E-3. . .